

GenCore version 5.1.6
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OM protein. - protein search, using sw model

Run on: March 11, 2005, 07:17:30 ; Search time 72.9307 Seconds
(without alignments)
4925.234 Million cell updates/sec

Title: US-10-027-400-2
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5652	100.0	1089	9	US-09-769-987-2
2	5652	100.0	1089	9	US-09-919-497-90
3	5652	100.0	1089	9	US-09-866-510-2
4	5652	100.0	1089	14	US-10-027-400-2
5	5652	100.0	1089	15	US-10-394-322A-50
6	5652	100.0	1089	15	US-10-367-639-35
7	5652	100.0	1089	16	US-10-322-696-168
8	5652	100.0	1089	16	US-10-741-601-439
9	5652	100.0	1089	17	US-10-741-600-1304
10	5649	99.9	1089	9	US-09-866-510-10
11	5648	99.9	1089	9	US-09-866-510-4
12	5648	99.9	1089	9	US-09-955-363-36
13	5647	99.9	1089	9	US-09-866-510-8

14	5646	99.9	1089	9	US-09-866-510-6	Sequence 6, Appli
15	5636.5	99.7	1088	10	US-09-961-403-4	Sequence 4, Appli
16	5232	92.6	1096	16	US-10-322-696-165	Sequence 165, App
17	3046	53.9	589	9	US-09-866-510-12	Sequence 12, Appl
18	2693.5	47.7	834	15	US-10-637-356-2	Sequence 2, Appli
19	2692	47.6	849	15	US-10-637-356-1	Sequence 1, Appli
20	2676.5	47.4	811	15	US-10-637-356-4	Sequence 4, Appli
21	2676.5	47.4	826	15	US-10-637-356-3	Sequence 3, Appli
22	2425	42.9	460	16	US-10-664-421-64	Sequence 64, Appl
23	2354.5	41.7	1106	9	US-09-866-510-22	Sequence 22, Appl
24	2354.5	41.7	1106	9	US-09-955-363-2	Sequence 2, Appli
25	2354.5	41.7	1106	15	US-10-394-322A-51	Sequence 51, Appl
26	2354.5	41.7	1106	15	US-10-367-639-36	Sequence 36, Appl
27	2351.5	41.6	1106	14	US-10-027-400-4	Sequence 4, Appli
28	2350.5	41.6	1106	9	US-09-866-510-16	Sequence 16, Appl
29	2349.5	41.6	1106	9	US-09-866-510-20	Sequence 20, Appl
30	2348.5	41.6	1106	9	US-09-866-510-18	Sequence 18, Appl
31	2347	41.5	1090	9	US-09-866-510-14	Sequence 14, Appl
32	2031	35.9	386	9	US-09-939-754-6	Sequence 6, Appli
33	2031	35.9	386	9	US-09-939-832-6	Sequence 6, Appli
34	2031	35.9	386	9	US-09-939-833-6	Sequence 6, Appli
35	1499.5	26.5	293	16	US-10-763-418-16	Sequence 16, Appl
36	1454.5	25.7	976	13	US-10-099-895-32	Sequence 32, Appl
37	1454.5	25.7	976	14	US-10-192-867-4	Sequence 4, Appli
38	1454.5	25.7	976	15	US-10-295-027-708	Sequence 708, App
39	1454.5	25.7	976	15	US-10-457-954-2	Sequence 2, Appli
40	1446.5	25.6	975	14	US-10-192-867-2	Sequence 2, Appli
41	1346.5	23.8	972	9	US-09-944-807-10	Sequence 10, Appl
42	1346.5	23.8	972	17	US-10-741-600-1570	Sequence 1570, Ap
43	1346.5	23.8	972	17	US-10-741-600-1571	Sequence 1571, Ap
44	1340.5	23.7	806	16	US-10-408-765A-2335	Sequence 2335, Ap
45	1287	22.8	1338	14	US-10-060-065-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
; FILE REFERENCE: 14014.0266U2
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 100.0%; Score 5652; DB 9; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60

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Db 121 VPDPDVAFVPLGMTDYLIVIVEDDDSAIIPCRITDPETPTLHNSGVVPASYDSRQGFNG 180
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Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN 240
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QY 1081 SDLVEDSFL 1089

Db 1081 SDLVEDSFL 1089
RESULT 2
US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US2002010662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-90
Query Match 100.0%; Score 5652; DB 9; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQLNSSFSLRCFGESEVSWQYP 60
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Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 3

US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-2

Query Match 100.0%; Score 5652; DB 9; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60
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Db 121 VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVPASYSRQGFNG 180
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Db 181 TFTVGPYICEATVKGKKFQTIPIPNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 240

Qy 241 EVVDLQWTPYGEVKGKIGITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
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Db 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
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Db 601 SGAFKXVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Qy 661 LGACTKSGPIYIIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYKKKSMMLDSEVKX 780
Db 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYKKKSMMLDSEVKX 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCWNSEPEKRPSEFVHLSEIVENLLPGQYKK 960
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Db 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 4

US-10-027-400-2
; Sequence 2, Application US/10027400
; Publication No. US20030017535A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market, Steuart Street Tower, 20th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,400
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,917
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-267-2-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-027-400-2

Query Match 100.0%; Score 5652; DB 14; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLCGLLTGLSLILCQLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLCGLLTGLSLILCQLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY 120
Qy 121 VPDPVAFVPLGMDYLVIVEDDSAILPCRTTDPETPVTLNHSEGVVPASYDSRQGFNG 180
Db 121 VPDPVAFVPLGMDYLVIVEDDSAILPCRTTDPETPVTLNHSEGVVPASYDSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKQFTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240
Db 181 TFTVGPYICEATVKGKQFTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240
Qy 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTILIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTILIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLLVIVII 540

Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVLG 600
Db 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVLG 600
Qy 601 SGAFGKVVEGTAYGLSRSQPMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPHLNIVNL 660
Db 601 SGAFGKVVEGTAYGLSRSQPMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPHLNIVNL 660
Qy 661 LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSYDIQRSLYDRPASYYKKKSMLDSEVK 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSYDIQRSLYDRPASYYKKKSMLDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYTKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYTKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDVPPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDIDVPPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 5

US-10-394-322A-50
; Sequence 50, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-50

Query Match 100.0%; Score 5652; DB 15; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLCGLLTGLSLILCQLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLCGLLTGLSLILCQLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY 120

Db 61 MSEEESDVEIRNEENNSGLFVTLEVSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120
QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVWPASYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVWPASYDSRQGFNG 180
QY 181 TFTVGPYICEATVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
QY 241 EVVDLQWTPYGEVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 300
Db 241 EVVDLQWTPYGEVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLENL 360
QY 361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLVLLV 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLVLLV 540
QY 541 SLIVLVVIWKQPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVIWKQPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV 660
Db 601 SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV 660
QY 661 LGACTKSGPIYIIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSDIQBSLYDRPASYKKKSMLDSEVK 780
Db 721 VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSDIQBSLYDRPASYKKKSMLDSEVK 780
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGMM 900
Db 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGMM 900
QY 901 VDSFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK 960
QY 961 SYEKIHLDFLKS DHPAARMRVDS DNAYIGVTYKNEEDKLKDWEGLDEORLSADSGYII 1020
Db 961 SYEKIHLDFLKS DHPAARMRVDS DNAYIGVTYKNEEDKLKDWEGLDEORLSADSGYII 1020
QY 1021 PLPDI DPVEEEDLGKRRHSSQTSEESA IETGSSSSTFKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDI DPVEEEDLGKRRHSSQTSEESA IETGSSSSTFKREDETIEDIDMDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

US-10-367-639-35
; Sequence 35, Application US/10367639
; Publication No. US20040001807A1
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Edelberg, Jay M.
; APPLICANT: Rafii, Shahin
; APPLICANT: Hong, Mun K.
; APPLICANT: Lanza, Robert P.
; APPLICANT: West, Michael D.
; TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular I
; FILE REFERENCE: 1676.004US1
; CURRENT APPLICATION NUMBER: US/10/367,639
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-639-35

Query Match 100.0%; Score 5652; DB 15; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60
QY 61 MSEEESDVEIRNEENNSGLFVTLEVSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTLEVSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120
QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVWPASYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVWPASYDSRQGFNG 180
QY 181 TFTVGPYICEATVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
QY 241 EVVDLQWTPYGEVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 300
Db 241 EVVDLQWTPYGEVKGKGFQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLENL 360
QY 361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLVLLV 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLVLLV 540
QY 541 SLIVLVVIWKQPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVIWKQPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV 660
Db 601 SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV 660
QY 661 LGACTKSGPIYIIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

QY 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVKN 780
Db |||||
QY 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVKN 780
Db |||||
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db |||||
QY 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYGM 900
Db |||||
QY 901 VDSFYNNKISGYRMAKPDHATSEVYIEMVKWCWNSEPEKRPSEVYHLSEIVENLLPGQYKK 960
Db |||||
QY 961 SYEKIHDLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db |||||
QY 1021 PLPDIDPVEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Db |||||
QY 1081 SDLVEDSFL 1089
Db |||||

RESULT 7

US-10-322-696-168
; Sequence 168, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-696-168

Query Match 100.0%; Score 5652; DB 16; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQLNSSFSRLRCFGESEVSWQYP 60
Db |||||
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120
Db |||||
QY 121 VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPTVLHNSGVVPASYSRQGFNG 180
Db |||||
QY 181 TFTVGPVCEATVKGKFKQFQIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
Db |||||
QY 241 EVVDLQWYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Db |||||

QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db |||||
QY 361 TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db |||||
QY 421 VDDHGSTGGQTVRCTAEGTLPDIEWMI CKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db |||||
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db |||||
QY 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
Db |||||
QY 601 SGAFKVVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660
Db |||||
QY 661 LGACTKSGPIYIIITEYCFYGDVNLVYHKNRDSFSLSHPEKPKKELDIFGLNPADESTRSY 720
Db |||||
QY 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVKN 780
Db |||||
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db |||||
QY 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYGM 900
Db |||||
QY 901 VDSFYNNKISGYRMAKPDHATSEVYIEMVKWCWNSEPEKRPSEVYHLSEIVENLLPGQYKK 960
Db |||||
QY 961 SYEKIHDLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db |||||
QY 1021 PLPDIDPVEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Db |||||
QY 1081 SDLVEDSFL 1089
Db |||||

RESULT 8

US-10-741-601-439
; Sequence 439, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 1089
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-10-741-601-439

Query Match      100.0%; Score 5652; DB 16; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
Db      1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy      61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120
Db      61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120

Qy      121 VPDPVAFVPLGMDTYLIVVEDDDSAIIPCRITDPETPTVLHNSGVVPASYDSRQGFNG 180
Db      121 VPDPVAFVPLGMDTYLIVVEDDDSAIIPCRITDPETPTVLHNSGVVPASYDSRQGFNG 180

Qy      181 TFTVGPICEATVGKGFQITPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db      181 TFTVGPICEATVGKGFQITPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Qy      241 EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db      241 EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300

Qy      301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIEN 360
Db      301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIEN 360

Qy      361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db      361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy      421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db      421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy      481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540
Db      481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Qy      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600
Db      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600

Qy      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600
Db      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600

Qy      601 SGAFKVVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660
Db      601 SGAFKVVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Qy      661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTSY 720
Db      661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTSY 720

Qy      721 VILSPENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYPASYKKKSMMLDSEVK 780
Db      721 VILSPENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYPASYKKKSMMLDSEVK 780

Qy      781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840
Db      781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

Qy      841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTPYPGNM 900
Db      841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTPYPGNM 900

Qy      901 VDSFTYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIIVENLLPGQYKK 960
Db      901 VDSFTYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIIVENLLPGQYKK 960

Qy      961 SYEKIHLDFLKS DHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db      961 SYEKIHLDFLKS DHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
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Db      961 SYEKIHLDFLKS DHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020

Qy      1021 PLPDIDPVPPEEDLGKRNHRHSQTSEESAIEATGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db      1021 PLPDIDPVPPEEDLGKRNHRHSQTSEESAIEATGSSSSTFIKREDETIEDIDMDDDIGIDS 1080

Qy      1081 SDLVEDSFL 1089
Db      1081 SDLVEDSFL 1089

RESULT 9
US-10-741-600-1304
; Sequence 1304, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1304
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1304

Query Match      100.0%; Score 5652; DB 17; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
Db      1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy      61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120
Db      61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYI 120

Qy      121 VPDPVAFVPLGMDTYLIVVEDDDSAIIPCRITDPETPTVLHNSGVVPASYDSRQGFNG 180
Db      121 VPDPVAFVPLGMDTYLIVVEDDDSAIIPCRITDPETPTVLHNSGVVPASYDSRQGFNG 180

Qy      181 TFTVGPICEATVGKGFQITPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db      181 TFTVGPICEATVGKGFQITPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Qy      241 EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db      241 EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300

Qy      301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIEN 360
Db      301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIEN 360

Qy      361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db      361 TEITTDVEKIQEIRYRSKLVIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy      421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db      421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy      481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540
Db      481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Qy      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600
Db      541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVLRVLG 600
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Qy	601	SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHLNIVNL	660
Db	601	SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHLNIVNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDVLVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDVLVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSYDRPASYYKKSMLDSEVK	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSYDRPASYYKKSMLDSEVK	780
Qy	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEFHYLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEFHYLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPPEEEDLGKRNHSSQTSEESAIEYGSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDPVPPEEEDLGKRNHSSQTSEESAIEYGSSSTFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089

RESULT 10
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: BRM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-10

Query Match	99.9%;	Score	5649;	DB	9;	Length	1089;
Best Local Similarity	99.9%;	Pred. No.	1.8e-311;				
Matches	1088;	Conservative	1;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	MGTSHAPFLVGLCLLTGLSLILCQLSLPILPNENEKVQLNSSFSRLRCFGESEVSWQYP	60				
Db	1	MGTSHAPFLVGLCLLTGLSLILCQLSLPILPNENEKVQLNSSFSRLRCFGESEVSWQYP	60				
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY	120				
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY	120				

Qy	121	VPDPDVAFVPLGMTDYLVIIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYSRQGFNG	180
Db	121	VPDPDVAFVPLGMTDYLVIIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKKFQIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICEATVKGKKFQIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLENL	360
Qy	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHGSTGGQTVRCTAEGPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD	480
Db	421	VDDHGSTGGQTVRCTAEGPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD	480
Qy	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII	540
Db	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII	540
Qy	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPNQLPYDSRWEFFPRDGLVLRVLG	600
Db	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPNQLPYDSRWEFFPRDGLVLRVLG	600
Qy	601	SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHLNIVNL	660
Db	601	SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHLNIVNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDVLVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDVLVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSYDRPASYYKKSMLDSEVK	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSYDRPASYYKKSMLDSEVK	780
Qy	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEFHYLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEFHYLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPPEEEDLGKRNHSSQTSEESAIEYGSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDPVPPEEEDLGKRNHSSQTSEESAIEYGSSSTFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089

RESULT 11
US-09-866-510-4
; Sequence 4, Application US/09866510
; Patent No. US20020111304A1

; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
us-09-866-510-4

Query Match 99.9%; Score 5648; DB 9; Length 1089;
Best Local Similarity 99.9%; Pred. No. 2.1e-311;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPILPNENEKVQLNSSFSRLCFGESEVSWQYP 60
Db 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPILPNENEKVQLNSSFSRLCFGESEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELEGRHIYIY 120

Qy 121 VPDPVAFVPLGMTDYLIVIVEDDDSAIIPCRITDPTPTVLHNSGVPASYSRQGFNG 180
Db 121 VPDPVAFVPLGMTDYLIVIVEDDDSAIIPCRITDPTPTVLHNSGVPASYSRQGFNG 180

Qy 181 TFTVGPYICEATVGKKFQTFIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TFTVGPYICEATVGKKFQTFIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Qy 241 EVVDLQWTPGEVKGKGIITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
Db 241 EVVDLQWTPGEVKGKGIITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

Qy 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL 360
Db 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL 360

Qy 361 TEITTDVEKIQEIRYRSKGLIRAKEEDSGHYTTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKGLIRAKEEDSGHYTTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGGTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGGTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy 481 RSTVEGRVTFKAVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA VLLVIVII 540
Db 481 RSTVEGRVTFKAVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA VLLVIVII 540

Qy 541 SLIVLVVWVKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWKFPRDGLVLRVLG 600
Db 541 SLIVLVVWVKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWKFPRDGLVLRVLG 600

Qy 601 SGAFKVVVEGTAYGLRSQPVKVAVMKLPKPTARSSEKQALMSELKIMTHLGPLHNI VNL 660
Db 601 SGAFKVVVEGTAYGLRSQPVKVAVMKLPKPTARSSEKQALMSELKIMTHLGPLHNI VNL 660

Qy 661 LGACTKSGPIYIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy 721 VILSFENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQVSLYDRPASYYKKSMMLDSEVK 780

Db 721 VILSFENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQVSLYDRPASYYKKSMMLDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAAGKIIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAAGKIIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYTKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYTKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAETGSSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAETGSSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 12
US-09-955-363-36
; Sequence 36, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; Bell, Lillian A.
; Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein									
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:									
US-09-955-363-36									
Query Match 99.9%; Score 5648; DB 9; Length 1089;									
Best Local Similarity 99.9%; Pred. No. 2.1e-311;									
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGTSHPAFVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP	60						
Db	1	MGTSHPAFVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP	60						
QY	61	MSEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120						
Db	61	MSEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120						
QY	121	VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPVTLHNSGVPVPSYDSRQGFNG	180						
Db	121	VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPVTLHNSGVPVPSYDSRQGFNG	180						
QY	181	TFTVGPYICEATVKGKFGITPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
Db	181	TFTVGPYICEATVKGKFGITPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
QY	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK	300						
Db	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK	300						
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360						
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360						
QY	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420						
Db	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420						
QY	421	VDDHHGSTGGQTVRCVCTAGTPLPDIEWMICKDIKKNNETSWTILANNVSNITTEIHSRD	480						
Db	421	VDDHHGSTGGQTVRCVCTAGTPLPDIEWMICKDIKKNNETSWTILANNVSNITTEIHSRD	480						
QY	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540						
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540						
QY	541	SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFPRDGLVLRVLG	600						
Db	541	SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFPRDGLVLRVLG	600						
QY	601	SGAFKVVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660						
Db	601	SGAFKVVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660						
QY	661	LGACTKSGPIYIIITEYCFYGDVNLHLKNRDLSFLSHHPEKPKKELDIFGLNPADESTSY	720						
Db	661	LGACTKSGPIYIIITEYCFYGDVNLHLKNRDLSFLSHHPEKPKKELDIFGLNPADESTSY	720						
QY	721	VILSFENNCDYMDMKQADTTQYVPMLEKKEVSKYSIQRSLYDRPASYYKKSMMLDSEVK	780						
Db	721	VILSFENNCDYMDMKQADTTQYVPMLEKKEVSKYSIQRSLYDRPASYYKKSMMLDSEVK	780						
QY	781	LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840						
Db	781	LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840						
QY	841	RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900						
Db	841	RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900						
QY	901	VDSTFVNKIKSGYRMKPDHATSEVYEIMVKNWSEPEKRPSPFHLSEIIVENLLPGQYKK	960						
Db	901	VDSTFVNKIKSGYRMKPDHATSEVYEIMVKNWSEPEKRPSPFHLSEIIVENLLPGQYKK	960						
QY	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII	1020						
Db	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII	1020						
QY	1021	PLPDIDPVPPEEDLGKRNHSSQTSEESAIETGSSSSTFIKREDETIEDIMDDIGIDS	1080						
Db	1021	PLPDIDPVPPEEDLGKRNHSSQTSEESAIETGSSSSTFIKREDETIEDIMDDIGIDS	1080						
QY	1081	SDLVEDSFL	1089						
Db	1081	SDLVEDSFL	1089						
RESULT 13									
US-09-866-510-8									
; Sequence 8, Application US/09866510									
; Patent No. US20020111304A1									
; GENERAL INFORMATION:									
; APPLICANT: KAZLAUSKAS, ANDRIUS									
; APPLICANT: IKUNO, YASUSHI									
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES									
; FILE REFERENCE: ERM-104.01									
; CURRENT APPLICATION NUMBER: US/09/866,510									
; CURRENT FILING DATE: 2001-05-25									
; PRIOR APPLICATION NUMBER: 60/250,747									
; PRIOR FILING DATE: 2000-12-01									
; PRIOR APPLICATION NUMBER: 60/289,103									
; PRIOR FILING DATE: 2001-05-07									
; NUMBER OF SEQ ID NOS: 33									
; SOFTWARE: PatentIn ver. 2.1									
; SEQ ID NO 8									
; LENGTH: 1089									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-866-510-8									
Query Match 99.9%; Score 5647; DB 9; Length 1089;									
Best Local Similarity 99.9%; Pred. No. 2.3e-311;									
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGTSHPAFVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP	60						
Db	1	MGTSHPAFVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP	60						
QY	61	MSEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120						
Db	61	MSEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120						
QY	121	VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPVTLHNSGVPVPSYDSRQGFNG	180						
Db	121	VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPVTLHNSGVPVPSYDSRQGFNG	180						
QY	181	TFTVGPYICEATVKGKFGITPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
Db	181	TFTVGPYICEATVKGKFGITPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
QY	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK	300						
Db	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK	300						
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360						
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360						
QY	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420						
Db	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420						
QY	421	VDDHHGSTGGQTVRCVCTAGTPLPDIEWMICKDIKKNNETSWTILANNVSNITTEIHSRD	480						
Db	421	VDDHHGSTGGQTVRCVCTAGTPLPDIEWMICKDIKKNNETSWTILANNVSNITTEIHSRD	480						
QY	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540						
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540						

Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540
Qy 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Qy 601 SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Db 601 SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Qy 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPHYHLSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPHYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEGTGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEGTGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 14

US-09-866-510-6
; Sequence 6, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-6
Query Match 99.9%; Score 5646; DB 9; Length 1089;
Best Local Similarity 99.9%; Pred. No. 2.7e-311;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSRLRCFGESEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Qy 121 VPDPAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSEGVVPASYSRQGFNG 180
Db 121 VPDPAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSEGVVPASYSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKKFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TFTVGPYICEATVKGKKFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN 240
Qy 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Db 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540
Qy 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Qy 601 SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Db 601 SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Qy 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPHYHLSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPHYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEGTGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEGTGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 15
US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

Query Match 99.7%; Score 5636.5; DB 10; Length 1088;
Best Local Similarity 99.9%; Pred. No. 9.2e-311;
Matches 1088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGTSHPAFLVLCGLLTGSLILCOLSLPSILPNEKVVQLNSSPSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLCGLLTGSLILCOLSLPSILPNEKVVQLNSSPSLRCFGESEVSWQYP 60

QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYI 120

QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTPTVLHNSGVPVPSYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTPTVLHNSGVPVPSYDSRQGFNG 180

QY 181 TFTVGPYICEATVKGKFKQITPENVVYALKATSELDEMEALKTIVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKFKQITPENVVYALKATSELDEMEALKTIVYKSGETIVVTCVFN 240

QY 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300

QY 301 EMKKVTVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLEN 360
Db 301 EMKKVTVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLEN 360

QY 361 TEITTDVEKIQEIYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

QY 421 VDDHGGSTGGTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGGSTGGTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVA AAVLVLLVIVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVA AAVLVLLVIVII 540

QY 541 SLIVLVVWQKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVWQKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600

QY 601 SGAFKVVVEGTAYGLSRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL 660
Db 601 SGAFKVVVEGTAYGLSRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL 660

QY 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

QY 721 VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSIQRSLYDRPASYYKKSMULDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSIQRSLYDRPASYYKKSMULDSEVKN 780

QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

QY 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPGMM 900

QY 901 VDSTFYNNKIKSGYRMAKPDHATSEVYIEMVKWNSEPEKRPSEYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNNKIKSGYRMAKPDHATSEVYIEMVKWNSEPEKRPSEYHLSEIVENLLPGQYKK 960

QY 961 SYEKIHLDFLKSHPAVARMVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARM-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1019

QY 1021 PLPDIDVPPEEEDLGKRNHRHSSQTSEESAIEGTSSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1020 PLPDIDVPPEEEDLGKRNHRHSSQTSEESAIEGTSSSSSTFIKREDETIEDIDMDDDIGIDS 1079

QY 1081 SDLVEDSFL 1089
Db 1080 SDLVEDSFL 1088

Search completed: March 11, 2005, 07:53:00
Job time : 77.9307 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 04:13:19 ; Search time 127.505 Seconds
(without alignments)
3303.265 Million cell updates/sec

Title: US-10-027-400-2
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5652	100.0	1089	5	AAU84300 Human end
2	5652	100.0	1089	6	ABG72449 Human pla
3	5652	100.0	1089	6	ABP96312 Human pla
4	5652	100.0	1089	7	ABR84718 Human PDG
5	5652	100.0	1089	7	ADF45081 Human kin
6	5652	100.0	1089	7	ADF90896 Human hep
7	5652	100.0	1089	8	ADM69012 Human pla
8	5652	100.0	1089	8	ADQ17833 Human sof
9	5652	100.0	1089	8	ADQ59532 Human can
10	5652	100.0	1089	8	ADQ39641 Human myo
11	5649	99.9	1089	2	AAR06910 Alpha typ
12	5649	99.9	1089	6	ABG72453 Human pla
13	5648	99.9	1089	6	ABG72450 Human pla
14	5647	99.9	1089	6	ABG72452 Human pla
15	5646	99.9	1089	6	ABG72451 Human pla
16	5645	99.9	1089	2	AAR08267 Platelet
17	5645	99.9	1089	8	ADM69031 Human PDG
18	5643	99.8	1089	8	ADM69014 Human PDG
19	5640	99.8	1089	8	ADM69035 Human PDG
20	5637	99.7	1090	8	ADM69020 Human PDG
21	5636.5	99.7	1088	5	AAO17356 Human pla
22	5617.5	99.4	1084	8	ADM69033 Human PDG
23	5617	99.4	1085	8	ADM69016 Human PDG
24	5614.5	99.3	1086	8	ADM69018 Human PDG
25	5602.5	99.1	1084	8	ADM69022 Human PDG

26	5533	97.9	1089	8	ADM69037	Adm69037 Human PDG
27	5232	92.6	1096	8	ADQ59529	Adq59529 Human can
28	5154	91.2	1009	2	AAR26206	Aar26206 Type B hu
29	3046	53.9	589	6	ABG72454	Abg72454 Human pla
30	2693.5	47.7	834	8	ADJ93550	Adj93550 NM_030917
31	2692	47.6	849	8	ADJ93549	Adj93549 NM_030917
32	2676.5	47.4	811	8	ADJ93552	Adj93552 NM_030917
33	2676.5	47.4	826	8	ADJ93551	Adj93551 NM_030917
34	2359.5	41.7	1106	2	AAR26205	Aar26205 Type B hu
35	2354.5	41.7	1106	1	AAP90127	Aap90127 Platelet
36	2354.5	41.7	1106	2	AAR99690	Aar99690 Platelet-
37	2354.5	41.7	1106	6	ABG72459	Abg72459 Human pla
38	2354.5	41.7	1106	6	ABP96311	Abp96311 Human pla
39	2354.5	41.7	1106	7	ABR84719	AbR84719 Human PDG
40	2354.5	41.7	1106	7	ADF45082	Adf45082 Human kin
41	2354.5	41.7	1106	8	ABO84679	Abo84679 Human can
42	2351	41.6	1107	8	ABO84677	Abo84677 Human can
43	2350.5	41.6	1106	6	ABG72456	Abg72456 Human pla
44	2349.5	41.6	1106	6	ABG72458	Abg72458 Human pla
45	2348.5	41.6	1106	6	ABG72457	Abg72457 Human pla

ALIGNMENTS

RESULT 1
AAU84300
ID AAU84300 standard; protein; 1089 AA.
XX
AC AAU84300;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human endometrial cancer related protein, PDGFRA.
XX
KW Human; endometrial cancer; differential expression; DNA microarray;
KW protein microarray.
XX
OS Homo sapiens.
XX
PN WO200209573-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US024104.
XX
PR 31-JUL-2000; 2000US-0221735P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI; 2002-179967/23.
DR N-PSDB; ABK35520.
XX
PT Diagnosing endometrial cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant endometrium.
XX
PS Claim 33; Page 214-217; 233pp; English.
XX
CC The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleic acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules selected from 50 fully defined sequences as given in the specification. The nucleic acids are used as an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen binding fragments, that specifically bind at least 2 different polypeptides from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are useful for the diagnosis of

DR WPI; 2003-268336/26.
XX New baculovirus having a modified genome encoding a therapeutic agent,
PT useful in the manufacture of a medicament for the treatment of cancer,
PT particularly prostate cancer.
XX Claim 33; Page; 34pp; English.
PS The present invention describes a humanised baculovirus (I) which
XX comprises a modified baculovirus genome having a nucleic acid molecule
CC encoding a therapeutic agent and a polypeptide which functions to target
CC the baculovirus to at least one cell type. Also described is a
CC pharmaceutical composition comprising (I). (I) has cytostatic activity,
CC and can be used in gene therapy. The baculovirus is useful in the
CC manufacture of a medicament for the treatment of cancer, particularly
CC prostate cancer. The present sequence represents the human platelet-
CC derived growth factor receptor alpha protein, which is specified in the
CC exemplification of the present invention. N.B. The present sequence is
CC not given in the specification but is referred to in Claim 33 as Genbank
CC accession number NM_006206
XX
SQ Sequence 1089 AA;
Query Match 100.0%; Score 5652; DB 6; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSHPAFLVGLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVGLGCLLTGLSLILCQLSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP 60
QY 61 MSEEESDVIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYIY 120
Db 61 MSEEESDVIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYIY 120
QY 121 VPDPDVAFPLGWTDLVIVEDDDSAIIPCRITDPTPTVLHNSGVPVPSYDSRQGFNG 180
Db 121 VPDPDVAFPLGWTDLVIVEDDDSAIIPCRITDPTPTVLHNSGVPVPSYDSRQGFNG 180
QY 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
Db 241 EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
QY 361 TEITTDVEKIQRYSRKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQRYSRKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHHGSTGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHHGSTGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLLRSELTVAAAVLLLVIVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLLRSELTVAAAVLLLVIVII 540
QY 541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
Db 541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
QY 601 SGAFKGVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNIVNL 660
Db 601 SGAFKGVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNIVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
XX

Db 661 LGACTKSGPIYIITEYCFYGDVLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSPFNNGDYMDMKQADTTQYVPMLEKEVSKYSYDIORSLYDRPASYYKKKSMMLDSEVKN 780
Db 721 VILSPFNNGDYMDMKQADTTQYVPMLEKEVSKYSYDIORSLYDRPASYYKKKSMMLDSEVKN 780
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPGWM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPGWM 900
QY 901 VDSTFYNKIKSGYRMAKPDHATSEVVEYIEMVKWCWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVVEYIEMVKWCWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020
QY 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGSSSTFIKREDETIEDIMMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGSSSTFIKREDETIEDIMMDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089
RESULT 4
ABR84718
ID ABR84718 standard; protein; 1089 AA.
XX
AC ABR84718;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PDGF alpha receptor protein.
XX
KW Tissue vascularisation; aging; mouse; human; PDGF A; PDGF B;
KW PDGF alpha receptor; PDGF beta receptor; endothelial precursor cell;
KW vascular disease; cardiant; cell therapy.
OS Homo sapiens.
XX
EN WO2003070083-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004244.
XX
PR 15-FEB-2002; 2002US-0357328P.
PR 08-AUG-2002; 2002WO-US025175.
XX
PA (CORR) CORNELL RES FOUND INC.
PA (EDEL/) EDELBERG J M.
PA (RAFI/) RAFII S.
PA (HONG/) HONG M K.
PA (LANZ/) LANZA R P.
PA (WEST/) WEST M D.
XX
PI Edelberg JM, Rafii S, Hong MK, Lanza RP, West MD;
XX
DR WPI; 2003-697548/66.
XX
PT Treating a vascular condition, e.g. myocardial infarction,
PT atherosclerosis, ischemia, congestive heart failure, hypertension,
PT stroke, thrombosis, arrhythmia or tachycardia, by administering
PT endothelial precursor cells.
XX
PS Claim 24; Page 47; 110pp; English.

Db	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQLNSSFSRLRCFGESEVSWQYP	60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY	120
QY	121	VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG	180
Db	121	VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG	180
QY	181	TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Db	181	TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
QY	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL	360
QY	361	TEITTDVEKIQEIRYRSKCLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIRYRSKCLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
QY	421	VDDHHGSTGGTVRCTAEGTPLPDIEWMICDKIKCNETSWTILANNVSNIIITEIHSRD	480
Db	421	VDDHHGSTGGTVRCTAEGTPLPDIEWMICDKIKCNETSWTILANNVSNIIITEIHSRD	480
QY	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII	540
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII	540
QY	541	SLIVLVITWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Db	541	SLIVLVITWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
QY	601	SGAFKGVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI	660
Db	601	SGAFKGVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI	660
QY	661	LGACTXSGPIYIIITEYCFYGDVNLVHLHKNRDLSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTXSGPIYIIITEYCFYGDVNLVHLHKNRDLSFLSHHPEKPKKELDIFGLNPADESTRSY	720
QY	721	VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRSLYDRPASYYKKSMMLDSEVK	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRSLYDRPASYYKKSMMLDSEVK	780
QY	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
QY	841	RDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVMSYGILLWEIFSLGGTYPYPGWM	900
Db	841	RDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVMSYGILLWEIFSLGGTYPYPGWM	900
QY	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSTFHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSTFHLSEIVENLLPGQYKK	960
QY	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
QY	1021	PLPDIDVPPEEEDLGKRRNRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDVPPEEEDLGKRRNRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS	1080
QY	1081	SDLVEDSFL	1089

Db	1081	SDLVEDSFL	1089
RESULT 6			
ADP90896			
ID	ADP90896	standard; protein; 1089 AA.	
XX			
AC	ADP90896;		
XX			
DT	26-FEB-2004	(first entry)	
XX			
DE	Human hepatic-fibrosis disease marker protein SEQ ID 358.		
XX			
KW	Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis; hepatic carcinoma; human.		
KW			
XX			
OS	Homo sapiens.		
XX			
PN	JP2003259877-A.		
XX			
PD	16-SEP-2003.		
XX			
PF	11-MAR-2002; 2002JP-00065013.		
XX			
PR	11-MAR-2002; 2002JP-00065013.		
XX			
PA	(SUMU) SUMITOMO SEIYAKU KK.		
XX			
DR	WPI; 2003-821598/77.		
XX			
PT	Hepatic fibrosis disease markers comprising polynucleotides or antibodies, useful for improved diagnosis, screening and developing drugs to treat hepatitis, to control cirrhosis and carcinoma.		
PT			
PT			
XX			
PS	Claim 3; SEQ ID NO 358; 313pp; Japanese.		
XX			
CC	The present invention relates to hepatic-fibrosis disease markers (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The sequences are useful for detecting and treating hepatic fibrosis caused by alcohol consumption, virus infection, etc., and the associated chronic hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The markers allow the cause of hepatic fibrosis to be clarified (diagnostic precision), so more suitable treatments can be developed and given.		
CC			
XX			
SQ	Sequence 1089 AA;		
Query Match 100.0%; Score 5652; DB 7; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQLNSSFSRLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQLNSSFSRLRCFGESEVSWQYP	60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY	120
QY	121	VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG	180
Db	121	VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG	180
QY	181	TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Db	181	TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
QY	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL	360

Qy	361	TEITTDVEKIQEIRYSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL	420
Db	361	TEITTDVEKIQEIRYSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL	420
Qy	421	VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII	TEIHSRD 480
Db	421	VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII	TEIHSRD 480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVL	LVLLVIVII 540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVL	LVLLVIVII 540
Qy	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGL	VLGRVLG 600
Db	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGL	VLGRVLG 600
Qy	601	SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGP	HLNIVNL 660
Db	601	SGAFKGVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGP	HLNIVNL 660
Qy	661	LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDIFGLNPADE	STRSY 720
Db	661	LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDIFGLNPADE	STRSY 720
Qy	721	VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSM	LDSEVK 780
Db	721	VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSM	LDSEVK 780
Qy	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIV	KICDFGLA 840
Db	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIV	KICDFGLA 840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSL	GGTPYPGMM 900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSL	GGTPYPGMM 900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKWCNSEPEKRPSEYHLSEIV	ENLLPGQYKK 960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKWCNSEPEKRPSEYHLSEIV	ENLLPGQYKK 960
Qy	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRL	SADSGYII 1020
Db	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRL	SADSGYII 1020
Qy	1021	PLPDIDVPPEEEDLGKRNHRHSSQTSSESIAETGSSSSTFIKREDETIED	IDMDDIGIDS 1080
Db	1021	PLPDIDVPPEEEDLGKRNHRHSSQTSSESIAETGSSSSTFIKREDETIED	IDMDDIGIDS 1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089
RESULT 7			
ADM69012			
ID	ADM69012	standard; protein; 1089 AA.	
XX			
AC	ADM69012;		
XX			
DT	03-JUN-2004	(first entry)	
XX			
DE	Human platelet derived growth factor receptor alpha wild-type	protein.	
XX			
KW	platelet derived growth factor receptor alpha; PDGFRA; neoplasia;	human;	
KW	type III receptor tyrosine kinase; Rtk; enzyme; receptor; wild-type.		
OS	Homo sapiens.		
XX			
PN	WO2003105773-A2.		
XX			
PD	24-DEC-2003.		
XX			

PF	13-JUN-2003;	2003WO-US018901.	
XX			
PR	13-JUN-2002;	2002US-0389107P.	
PR	08-JAN-2003;	2003US-0438899P.	
XX			
PA	(UYOR-) UNIV OREGON HEALTH SCI.		
PA	(DAND) DANA FARBER CANCER INST INC.		
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
PA	(USGO) US DEPT VETERANS AFFAIRS.		
XX			
PI	Heinrich MC, Corless CL, Fletcher JA, Demetri GD;		
XX			
DR	WPI; 2004-082052/08.		
DR	N-PSDB; ADM69011, ADM69029.		
XX			
PT	New isolated variant platelet derived growth factor alpha (PDGFRA)		
PT	polypeptide, useful for screening for a compound useful in influencing		
PT	PDGFRA-mediated neoplasia in a mammal.		
XX			
PS	Example 1; SEQ ID NO 2; 302pp; English.		
XX			
CC	The invention relates to a novel isolated variant platelet derived growth		
CC	factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the		
CC	invention is a type III receptor tyrosine kinase (RTK) and may be useful		
CC	for screening for a compound that may influence PDGFRA-mediated neoplasia		
CC	in a mammal. The current sequence is that of the human PDGFRA wild-type		
CC	protein of the invention.		
XX			
SQ	Sequence 1089 AA;		
Query Match 100.0%; Score 5652; DB 8; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MGTSHPAFLVLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSILRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSILRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENELEGRHIYIY	120
Qy	121	VPDPVAFVPLGMTDYLVIIVEDDDSAIIPCRITDPETVTLHNSGVVPASYSRQGFNG	180
Db	121	VPDPVAFVPLGMTDYLVIIVEDDDSAIIPCRITDPETVTLHNSGVVPASYSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKQFQITPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN	240
Db	181	TFTVGPYICEATVKGKQFQITPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN	240
Qy	241	EVVDLQWTPYGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Db	241	EVVDLQWTPYGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNLTLIEN	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNLTLIEN	360
Qy	361	TEITTDVEKIQEIRYSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL	420
Db	361	TEITTDVEKIQEIRYSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL	420
Qy	421	VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII	TEIHSRD 480
Db	421	VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII	TEIHSRD 480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVL	LVLLVIVII 540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVL	LVLLVIVII 540
Qy	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGL	VLGRVLG 600
Db	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGL	VLGRVLG 600

QY 601 SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Db 601 SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVNLVYLHKNRDSFLSHHPEKPKKELDFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVYLHKNRDSFLSHHPEKPKKELDFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKSMMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKSMMLDSEVKN 780
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGMM 900
QY 901 VDSTFYNKISGYRMAKPDHATSEVVEIMVKWCWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKISGYRMAKPDHATSEVVEIMVKWCWNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
QY 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
QY 1021 PLPDIDVPBEEDLGKRRHSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDVPBEEDLGKRRHSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 8
ADQ17833
ID ADQ17833 standard; protein; 1089 AA.
XX
AC ADQ17833;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 650.
XX
KW soft tissue sarcoma; cytotostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 650; 210pp; English.
XX

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytotostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1089 AA;

Query Match 100.0%; Score 5652; DB 8; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches-1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPSILPNENEKVQQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPSILPNENEKVQQLNSSFSRLRCFGESEVSWQYP 60
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
QY 121 VPDPDVAFVPLGMDTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG 180
QY 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSETIVVTCVFN 240
QY 241 EVVDLQWTPYGEVKGKITMLLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Db 241 EVVDLQWTPYGEVKGKITMLLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
QY 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISWLKNNLTLENL 360
Db 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISWLKNNLTLENL 360
QY 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
QY 541 SLIVLVIWKQKPRYIEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVIWKQKPRYIEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Db 601 SGAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVNLVYLHKNRDSFLSHHPEKPKKELDFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVYLHKNRDSFLSHHPEKPKKELDFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKSMMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKSMMLDSEVKN 780
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDimHDSNYVSKGSTFLPVKWMAPESIFDNLyTTLSDVWSYGILLWEIFSLGGTPYPCGM 900
Db 841 RDimHDSNYVSKGSTFLPVKWMAPESIFDNLyTTLSDVWSYGILLWEIFSLGGTPYPCGM 900
Qy 901 VDSTfYnKIKSGYrMAKPDHATSEVYEIMVKcWNSEPEKRPsfYHLSEIvENLLPGQYKk 960
Db 901 VDSTfYnKIKSGYrMAKPDHATSEVYEIMVKcWNSEPEKRPsfYHLSEIvENLLPGQYKk 960
Qy 961 SYEKIHLDfLKSdHPAvmRVDSdNAYIGvTYKNEEDKLKdWEGGLdEQRLSADSGYII 1020
Db 961 SYEKIHLDfLKSdHPAvmRVDSdNAYIGvTYKNEEDKLKdWEGGLdEQRLSADSGYII 1020
Qy 1021 PLPDIDpVPEEDLGKRnRHSSQTSESAIETGSSSSTfIKREdETIEDIdMDDIGIDS 1080
Db 1021 PLPDIDpVPEEDLGKRnRHSSQTSESAIETGSSSSTfIKREdETIEDIdMDDIGIDS 1080
Qy 1081 SdLVeDSfL 1089
Db 1081 SdLVeDSfL 1089

RESULT 9
ADQ59532
ID ADQ59532 standard; protein; 1089 AA.
XX
AC ADQ59532;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer-associated (CA) protein sequence SEQ ID NO:168.
XX
KW human; cancer-associated gene; cancer-associated protein; cytostatic;
KW gene therapy; vaccine; tyrosine kinase antagonist;
KW G-protein coupled receptor antagonist; cancer; lymphoma.
XX
OS Homo sapiens.
XX
PN WO2004058288-A1.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040082.
XX
PR 17-DEC-2002; 2002US-00322696.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543349/52.
DR N-PSDB; ADQ59530, ADQ59531.
XX
PT New cancer-associated nucleic acid for diagnosing, preventing or treating
PT cancer (e.g. lymphoma) or for screening agents that may be used for
PT treating or preventing cancer.
XX
PS Claim 19; SEQ ID NO 168; 143pp; English.
XX
CC The present invention describes human cancer-associated (CA) nucleotide
CC sequences (I). Also described: (1) an expression vector comprising (I);
CC (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC within an open reading frame of a CA sequence; (5) an isolated antibody,
CC or its antigen binding fragment, that binds to the above polypeptide; (6)
CC a hybridoma that produces the monoclonal antibody described above; (7) a
CC pharmaceutical composition comprising the antibody and a pharmaceutical
CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC the above (monoclonal) antibody or polynucleotide that selectively
CC hybridises to any of the polynucleotide sequences mentioned above; (9)
CC methods for diagnosing cancer or for detecting the presence or absence of

CC cancer cells in an individual; (10) a method for inhibiting growth of
CC cancer cells in an individual; (11) a method for delivering a therapeutic
CC agent to cancer cells in an individual; (12) an electronic library
CC comprising the polynucleotide or polypeptide, or their fragments,
CC mentioned above; (13) a method of screening for anticancer activity; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC or the presence of the antibody in a test cell or serum sample; (15) a
CC method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein encoded by the above nucleic acid molecule; and
CC (16) a method for treating cancers. (I) has cytostatic activity, and can
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC and as a G-protein coupled receptor antagonist. The compositions and
CC methods of the present invention can be used for diagnosing, preventing
CC and treating cancer, especially lymphomas. They may also be used in
CC screening for agents that may be used for treating or preventing cancer.
CC The present sequence represents a human CA gene amino acid sequence,
CC which is given in the exemplification of the present invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1089 AA;

Query Match 100.0%; Score 5652; DB 8; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILQSLPSILPNENEKVQLNSSFSRLCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILQSLPSILPNENEKVQLNSSFSRLCFGESEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120

Qy 121 VDPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPETPTVLHNSGWWPASYDSRQGFNG 180
Db 121 VDPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPETPTVLHNSGWWPASYDSRQGFNG 180

Qy 181 TFTVGPYICEATVKGKKFQTFIPFNYYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKKFQTFIPFNYYALKATSELDEMEALKTVYKSGETIVVTCVFN 240

Qy 241 EVVDLQWTPGGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDGDYECARQATREV 300
Db 241 EVVDLQWTPGGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDGDYECARQATREV 300

Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIEN 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIEN 360

Qy 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR 480
Db 421 VDDHGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR 480

Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLPSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLPSELTVAAAVLVLVIVII 540

Qy 541 SLIVLVVIWKQKPRYERIRWVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
Db 541 SLIVLVVIWKQKPRYERIRWVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600

Qy 601 SGAFGKVVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660
Db 601 SGAFGKVVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Qy 661 LGACTKSGPIYIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db 661 LGACTSGPIYIITEYCFYGDVLNVLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSLYDRPASYYKKSMLDSEVK 780

Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKEVSKYSDIQRLSLYDRPASYYKKSMLDSEVK 780

Qy 781 LLSDDNSEGLTLDDLSTFYQVARGNEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

Db 781 LLSDDNSEGLTLDDLSTFYQVARGNEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900

Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900

Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFYLSEIVENLLPGQYKK 960

Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFYLSEIVENLLPGQYKK 960

Qy 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy 1021 PLPDIDPVEEEDLGKRNHRSSQTSSESIAIETGSSSSTFIKREDETIEDIMMDDIGIDS 1080

Db 1021 PLPDIDPVEEEDLGKRNHRSSQTSSESIAIETGSSSSTFIKREDETIEDIMMDDIGIDS 1080

Qy 1081 SDLVEDSFL 1089

Db 1081 SDLVEDSFL 1089

RESULT 10

ADQ39641

ID ADQ39641 standard; protein; 1089 AA.

XX

AC ADQ39641;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1304.

XX

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiant; gene therapy; human.

XX

OS Homo sapiens.

XX

PN WO2004058052-A2.

XX

PD 15-JUL-2004.

XX

PF 22-DEC-2003; 2003WO-US040978.

XX

PR 20-DEC-2002; 2002US-0434778P.

PR

PR 10-MAR-2003; 2003US-0453135P.

PR

PR 30-APR-2003; 2003US-0466412P.

PR

PR 23-SEP-2003; 2003US-0504955P.

XX

PA (APPL-) APPLERA CORP.

XX

PI Cargill M, Devlin JJ, Iakoubova O;

XX

XX WPI; 2004-533949/51.

DR

DR N-PSDB; ADQ38813.

XX

XX Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX

PS Claim 10; SEQ ID NO 1304; 145pp; English.

XX

CC The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide

CC comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the

CC polynucleotide, a buffer and an enzyme; a method of detecting a variant

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNP's of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

XX

SQ Sequence 1089 AA;

Query Match 100.0%; Score 5652; DB 8; Length 1089;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60

Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTCYNNHTQTEENELEGRHIYIY 120

Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTCYNNHTQTEENELEGRHIYIY 120

Qy 121 VDDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPTLHNSGVWPASYDSRQGFNG 180

Db 121 VDDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPTLHNSGVWPASYDSRQGFNG 180

Qy 181 TFTVGPYICEATVKGKFKQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240

Db 181 TFTVGPYICEATVKGKFKQTFIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240

Qy 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVTLTVPEATVKDSGDYECARQATREV 300

Db 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVTLTVPEATVKDSGDYECARQATREV 300

Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP PPRISWLKNNLTLIENL 360

Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP PPRISWLKNNLTLIENL 360

Qy 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Db 361 TEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Db 421 VDDHGGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTILRSELTVAAAVLLLVII 540

Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTILRSELTVAAAVLLLVII 540

Qy 541 SLIVLVVIWKQKPRYEIRNRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600

Db 541 SLIVLVVIWKQKPRYEIRNRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600

Qy 601 SGAFKGVWEGTAYGLSRSQPMKAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Db	601	SGAFGKVVECTAYGLSRSPVMKVAVQMLKPTARSSSEKQALMSELKIMTHLGPHLNIVNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDLVNVLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDLVNVLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY	720
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYYKKSMLDSEVKN	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYYKKSMLDSEVKN	780
Qy	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGWM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGWM	900
Qy	901	VDSTFYNNKIKSGYRMAKPDHATSEVYEIMVKWCWNSEPEKRPSEFYLSEIIVENLLPGQYKK	960
Db	901	VDSTFYNNKIKSGYRMAKPDHATSEVYEIMVKWCWNSEPEKRPSEFYLSEIIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVEEEDLGKRRHSSQTSESAETGSSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDPVEEEDLGKRRHSSQTSESAETGSSSSTFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089
RESULT 11			
AAR06910			
ID	AAR06910 standard; protein; 1089 AA.		
xx			
AC	AAR06910;		
xx			
DT	25-MAR-2003 (revised)		
DT	16-JAN-1991 (first entry)		
xx			
DE	Alpha type PDGF receptor deduced from TR4 cDNA clone.		
xx			
KW	platelet derived growth factor; T11.		
xx			
OS	Homo sapiens.		
xx			
FH	Key		
FT	Domain	Location/Qualifiers	
FT		1..23	
FT		/label= signal peptide	
FT	Domain	24..524	
FT		/label= ligand binding domain	
FT	Modified-site	42..44	
FT	Modified-site	/label= N-glycos_site	
FT		76..78	
FT		/label= N-glycos_site	
FT	Modified-site	103..105	
FT		/label= N-glycos_site	
FT	Modified-site	179..181	
FT		/label= N-glycos_site	
FT	Modified-site	353..355	
FT		/label= N-glycos_site	
FT	Modified-site	359..361	
FT		/label= N-glycos_site	
FT	Modified-site	458..460	
FT		/label= N-glycos_site	
FT	Modified-site	468..470	
FT		/label= N-glycos_site	
FT	Domain	525..548	
FT		/label= transmembrane region	

Domain	549..599																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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CC	diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC	atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC	scleroderma, keloids, hypertrophic scars, skin wound healing or
CC	proliferative vitreoretinopathy). The method may be used in identifying
CC	compounds for treating or preventing the development of diseases
CC	involving cell contraction, e.g. fibrotic diseases. This is the amino
CC	acid sequence of human platelet derived growth factor receptor (PDGFR)
CC	alpha mutant V859M
XX	
SQ	Sequence 1089 AA;
Query Match 99.9%; Score 5649; DB 6; Length 1089;	
Best Local Similarity 99.9%; Pred. No. 0;	
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGTSHPAFLVGLGCLLTGLSLILCQLSLPSILPNENEKVQVQLNSPFLRCFGESEVSWQYP 60
Db	1 MGTSHPAFLVGLGCLLTGLSLILCQLSLPSILPNENEKVQVQLNSPFLRCFGESEVSWQYP 60
Qy	61 MSEEESDVBEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYIY 120
Db	61 MSEEESDVBEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYVNHQTQTEENELEGRHIYIY 120
Qy	121 VPDPDVAFVPLGMTDYLIVIVEDDDSAIIPCRITTDPTPTVLHNSGVPVASYDSRQGFNG 180
Db	121 VPDPDVAFVPLGMTDYLIVIVEDDDSAIIPCRITTDPTPTVLHNSGVPVASYDSRQGFNG 180
Qy	181 TFTVGPVCEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
Db	181 TFTVGPVCEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240
Qy	241 EVVDLOWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Db	241 EVVDLOWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Qy	301 EMKVTITSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLIENL 360
Db	301 EMKVTITSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLIENL 360
Qy	361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db	361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy	421 VDDHGSTGGQTVRCTAEGTPLPDIEWNICDKIKCNETSWTILANNVSNIIITEIHSRD 480
Db	421 VDDHGSTGGQTVRCTAEGTPLPDIEWNICDKIKCNETSWTILANNVSNIIITEIHSRD 480
Qy	481 RSTVEGRVTPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db	481 RSTVEGRVTPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy	541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVGRVLG 600
Db	541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFPRDGLVGRVLG 600
Qy	601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI 660
Db	601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI 660
Qy	661 LGACTKSGPIYIITEYCFYGDVLVYLHNKRDVFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db	661 LGACTKSGPIYIITEYCFYGDVLVYLHNKRDVFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy	721 VILSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSDIQVSLYDRPASYKKKMLDSEVK 780
Db	721 VILSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSDIQVSLYDRPASYKKKMLDSEVK 780
Qy	781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db	781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy	841 RDIMHDSNVYSGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGCTPPPGMM 900

Db	841 RDIMHDSNVYSGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGCTPPPGMM 900
Qy	901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFHLSEIVENLLPGQYKK 960
Db	901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFHLSEIVENLLPGQYKK 960
Qy	961 SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db	961 SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy	1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAETGSSSSTFIKREDETIEDIMDDDIGIDS 1080
Db	1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAETGSSSSTFIKREDETIEDIMDDDIGIDS 1080
Qy	1081 SDLVEDSFL 1089
Db	1081 SDLVEDSFL 1089
RESULT 13	
ABG72450	
ID	ABG72450 standard; protein; 1089 AA.
XX	
AC	ABG72450;
XX	
DT	13-FEB-2003 (first entry)
XX	
DE	Human platelet derived growth factor receptor alpha mutant E587K.
XX	
KW	Human; platelet derived growth factor receptor alpha; PDGFRalpha; hepatotropic; dermatological; nephrotropic; vulnery; ophthalmological; cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3; phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation; cell migration; extracellular matrix synthesis; secretion; cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis; liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma; keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; mutant; mutein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Domain 1..490
FT	/label= Extracellular_domain
FT	Peptide 1..24
FT	/label= Signal_peptide_sequence_2
FT	Peptide 1..20
FT	/label= Signal_peptide_sequence_1
FT	Protein 21
FT	/label= Mature_PDGFR_sequence_1
FT	Protein 25
FT	/label= Mature_PDGFR_sequence_2
FT	Domain 42..102
FT	/label= Immunoglobulin-like_domain
FT	Domain 143..191
FT	/label= Immunoglobulin-like_domain
FT	Domain 228..292
FT	/label= Immunoglobulin-like_domain
FT	Domain 338..399
FT	/label= Immunoglobulin-like_domain
FT	/note= "6"
FT	Domain 428..503
FT	/label= Immunoglobulin-like_domain
FT	Domain 525..548
FT	/label= Transmembrane_domain
FT	Domain 549..1055
FT	/label= Intracellular_domain
FT	Domain 556..661
FT	/note= "Split tyrosine kinase domain segment 1"
FT	Misc-difference 587
FT	/note= "Wild type Glu substituted by Lys"
FT	Domain 760..900

FT	/note= "Split tyrosine kinase domain segment 2"	
XX	PN	US2002111304-A1.
XX	PD	15-AUG-2002.
XX	PF	25-MAY-2001; 2001US-00866510.
XX	PR	01-DEC-2000; 2000US-0250747P.
PR	PR	07-MAY-2001; 2001US-0289103P.
XX		
PA	PA	(KAZL/) KAZLAUSKAS A.
XX	XX	(IKUN/) IKUNO Y.
PI		Kazlauskas A, Ikuno Y;
XX		WPI; 2003-066697/06.
DR		N-PSDB; ABS57781.
XX		
PPT	New polypeptide for treating or preventing diseases associated with an	
PPT	abnormal platelet-derived growth factor (PDGF) level, e.g. cell	
PPT	proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha	
PT	or -beta.	
XX		
PS	Claim 7; Page 45-47; 127pp; English.	
XX		
CC	The invention describes a polypeptide comprising a portion of the	
CC	receptor tyrosine kinase platelet-derived growth factor alpha receptor	
CC	(PDGFalpha). The polypeptide and the polynucleotide are useful in	
CC	treating or preventing diseases and conditions associated with an	
CC	abnormal PDGF level or response, such as cell proliferation, cell	
CC	migration, extracellular matrix synthesis and secretion or cell	
CC	contraction. Exemplary diseases or disorders include cell proliferative	
CC	diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.	
CC	atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,	
CC	scleroderma, keloids, hypertrophic scars, skin wound healing or	
CC	proliferative vitreoretinopathy). The method may be used in identifying	
CC	compounds for treating or preventing the development of diseases	
CC	involving cell contraction, e.g. fibrotic diseases. This is the amino	
CC	acid sequence of human platelet derived growth factor receptor (PDGFR)	
CC	alpha mutant E587K	
XX		
SQ	Sequence 1089 AA;	
	Query Match	99.9%; Score 5648; DB 6; Length 1089;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 1088; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
QY	1	MGTSHPAFVLVGLCLLTGLSLILCOLSLPSILPNENEKVQLNSSFSLRCFGESEVSWQYP 60
DB	1	MGTSHPAFVLVGLCLLTGLSLILCOLSLPSILPNENEKVQLNSSFSLRCFGESEVSWQYP 60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY 120
DB	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIY 120
QY	121	VPDPDVAFVPLGMTDYLIVVEDDDSAIIPCRITDPETPVLHNSGVPASYDSRQGFNG 180
DB	121	VPDPDVAFVPLGMTDYLIVVEDDDSAIIPCRITDPETPVLHNSGVPASYDSRQGFNG 180
QY	181	TFTVGPYICEATVKGKQFQIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
DB	181	TFTVGPYICEATVKGKQFQIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY	241	EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
DB	241	EVVDLQWTPGVEVGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPIRISWLKNNLTLIENL 360
DB	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPIRISWLKNNLTLIENL 360
QY	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Db	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy	421	VDDHHGSTGGQTVRCTAEGTPLPDIEMWICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db	421	VDDHHGSTGGQTVRCTAEGTPLPDIEMWICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Qy	541	SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVLG 600
Db	541	SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWKFPDRDGLVLRVLG 600
Qy	601	SGAFGKVEGTAYGLRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
Db	601	SGAFGKVEGTAYGLRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
Qy	661	LGACTKSGPIYIIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db	661	LGACTKSGPIYIIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy	721	VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
Db	721	VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
Qy	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGVM 900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGVM 900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKEPSPFYHLSEIVENLLPGQYKK 960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKEPSPFYHLSEIVENLLPGQYKK 960
Qy	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVITYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db	961	SYEKIHLDFLKSHPAVARMRVDSDNAYIGVITYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy	1021	PLPDIDPVPPEEDLGKRNHSSQTSEESAETGSSSSTFIKREDETIEDIMDDDIGIDS 1080
Db	1021	PLPDIDPVPPEEDLGKRNHSSQTSEESAETGSSSSTFIKREDETIEDIMDDDIGIDS 1080
Qy	1081	SDLVEDSFL 1089
Db	1081	SDLVEDSFL 1089
RESULT 14		
ABG72452		
ID	ABG72452 standard; protein; 1089 AA.	
XX		
AC	ABG72452;	
XX		
DT	13-FEB-2003 (first entry)	
XX		
DE	Human platelet derived growth factor receptor alpha mutant D818N.	
XX		
KW	Human; platelet derived growth factor receptor alpha; PDGFRalpha;	
KW	hepatotropic; dermatological; nephrotropic; vulnery; ophthalmological;	
KW	cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;	
KW	phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;	
KW	cell migration; extracellular matrix synthesis; secretion;	
KW	cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;	
KW	liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;	
KW	keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;	
XX	mutant; mutin.	
XX		
OS	Homo sapiens.	

OS Synthetic.
XX Key
FH Domain
FT Location/Qualifiers
FT 1. .490
FT /label= Extracellular_domain
FT 1. .24
FT /label= Signal_peptide_sequence_2
FT 1. .20
FT /label= Signal_peptide_sequence_1
FT 21
FT /label= Mature_PDGF_ sequence_1
FT 25
FT /label= Mature_PDGF_ sequence_2
FT 42. .102
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FT 525. .548
FT /label= Transmembrane_domain
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FT /label= Intracellular_domain
FT 556. .661
FT /note= "Split tyrosine kinase domain segment 1"
FT 760. .900
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FT Misc-difference 818
FT /note= "Wild type Asp substituted by Asn"
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PD 15-AUG-2002.
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PF 25-MAY-2001; 2001US-00866510.
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PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
XX
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
XX
PI Kazlauskas A, Ikuno Y;
XX
XX WPI; 2003-066697/06.
DR N-PSDB; ABS57783.
DR
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 58-60; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)

CC alpha mutant D818N
XX
SQ Sequence 1089 AA;
Query Match 99.9%; Score 5647; DB 6; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 121 VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVTLHNSGVVPASYSRQGFNG 180
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Qy 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLSBELTVAAAVLVLVIVII 540
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Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089
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AC ABG72451;
XX
DT 13-FEB-2003 (first entry)
XX Human platelet derived growth factor receptor alpha mutant T665M.
DE
KW Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW hepatotropic; dermatological; nephrotropic; vulnery; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW liver cirrhosis; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW mutant; muten.
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OS Homo sapiens.
OS Synthetic.
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FT Domain 760..900
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PN US2002111304-A1.
XX
PD 15-AUG-2002.
XX
PF 25-MAY-2001; 2001US-00866510.

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PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
XX
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
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DR WPI; 2003-066697/06.
DR N-PSDB; ABS57782.
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 51-54; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalpha). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)
CC alpha mutant T665M
XX
SQ Sequence 1089 AA;
Query Match 99.9%; Score 5646; DB 6; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGTSHPAFLVLGCLLTGLSLILQSLPSILPNENEKVQNLNSSFSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILQSLPSILPNENEKVQNLNSSFSLRCFGESEVSWQYP 60
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Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYI 120
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Qy	1081	SDLVEDSFL	1089			
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Db	1081	SDLVEDSFL	1089			

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:10:35 ; Search time 31.7522 Seconds
(without alignments)
2560.230 Million cell updates/sec

Title: US-10-027-400-2
Perfect score: 5652
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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5652	100.0	1089	2	US-08-460-510-4 Sequence 4, Appli
3	5652	100.0	1089	2	US-08-460-490-4 Sequence 4, Appli
4	5652	100.0	1089	3	US-08-462-728-2 Sequence 2, Appli
5	5652	100.0	1089	3	US-08-461-917-2 Sequence 2, Appli
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8	5652	100.0	1089	4	US-09-769-987-2 Sequence 2, Appli
9	5652	100.0	1089	4	US-09-866-510-2 Sequence 2, Appli
10	5652	100.0	1089	4	US-09-919-497-90 Sequence 90, Appl
11	5652	100.0	1089	4	US-09-949-016-6703 Sequence 6703, Ap
12	5652	100.0	1089	5	PCT-US92-00730-4 Sequence 4, Appli
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14	5649	99.9	1089	4	US-09-866-510-10 Sequence 10, Appl
15	5648	99.9	1089	1	US-08-180-195-36 Sequence 36, Appl
16	5648	99.9	1089	1	US-08-477-329-36 Sequence 36, Appl
17	5648	99.9	1089	2	US-08-475-458-36 Sequence 36, Appl
18	5648	99.9	1089	3	US-08-980-400-36 Sequence 36, Appl
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20	5648	99.9	1089	3	US-09-583-210-36 Sequence 36, Appl
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24	5647	99.9	1089	4	US-09-866-510-8 Sequence 8, Appli
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31	2354.5	41.7	1106	2	US-08-475-458-2	Sequence 2, Appli
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34	2354.5	41.7	1106	3	US-09-583-210-2	Sequence 2, Appli
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42	2351.5	41.6	1106	3	US-08-461-917-4	Sequence 4, Appli
43	2351.5	41.6	1106	4	US-08-464-436-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 4, Application US/08168917
; Patent No. 5686572
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-168-917-4

Query Match 100.0%; Score 5652; DB 1; Length 1089;

Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	421	VDDHGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWTILANNVSNIIIEIHSRD	480						
Qy	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLLLVIVII	540						
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLLLVIVII	540						
Qy	541	SLIVLVVWVKQPRYEIRWRVIESISPDGHEIYIYVDPMLPQYDSRWEFPRDGLVGRVLG	600						
Db	541	SLIVLVVWVKQPRYEIRWRVIESISPDGHEIYIYVDPMLPQYDSRWEFPRDGLVGRVLG	600						
Qy	601	SGAFKVVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660						
Db	601	SGAFKVVVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660						
Qy	661	LGACTKSGPIYIITEYCFYGDVNLHLKNRDLSFLSHHPEKPKKELDIFGLNPADESTRSY	720						
Db	661	LGACTKSGPIYIITEYCFYGDVNLHLKNRDLSFLSHHPEKPKKELDIFGLNPADESTRSY	720						
Qy	721	VILSFENNGDYMCKQADTTQYVPMLEKVEVSKYSDIQRLSLYDRPASYYKKSMLDSEVK	780						
Db	721	VILSFENNGDYMCKQADTTQYVPMLEKVEVSKYSDIQRLSLYDRPASYYKKSMLDSEVK	780						
Qy	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840						
Db	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840						
Qy	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900						
Db	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900						
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSEFHLSEIIVENLLPGQYKK	960						
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSEFHLSEIIVENLLPGQYKK	960						
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020						
Db	961	SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII	1020						
Qy	1021	PLPDIDPVEEEDLGKRRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMDDDIGIDS	1080						

Db	1021	PLPDIDPVEEEDLGKRRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMDDDIGIDS	1080						
Qy	1081	SDLVEDSFL	1089						
Db	1081	SDLVEDSFL	1089						
RESULT 2									
US-08-460-510-4									
; Sequence 4, Application US/08460510									
; Patent No. 5872218									
; GENERAL INFORMATION:									
; APPLICANT: Wolf, David									
; APPLICANT: Tomlinson, James E.									
; APPLICANT: Fretto, Larry J.									
; APPLICANT: Giese, Neill A.									
; APPLICANT: Escobedo, Jaime A.									
; APPLICANT: Williams, Lewis T.									
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN									
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES									
; NUMBER OF SEQUENCES: 23									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW									
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000									
; CITY: San Francisco									
; STATE: California									
; COUNTRY: US									
; ZIP: 94105									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: PatentIn Release #1.0, Version #1.25									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/460,510									
; FILING DATE: 02-JUN-1995									
; CLASSIFICATION: 435									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Dow, Karen B.									
; REGISTRATION NUMBER: 29,684									
; REFERENCE/DOCKET NUMBER: 012418-001430									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (415) 326-2400									
; TELEFAX: (415) 326-2422									
; INFORMATION FOR SEQ ID NO: 4:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 1089 amino acids									
; TYPE: amino acid									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
US-08-460-510-4									
Query Match 100.0%; Score 5652; DB 2; Length 1089;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP	60						
Db	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP	60						
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYI	120						
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYI	120						
Qy	121	VPDPDVAFPVLGMDTYLVIVEDDDSAIIPCRITDPETPVTILHNSEGVPASYSRQGFNG	180						
Db	121	VPDPDVAFPVLGMDTYLVIVEDDDSAIIPCRITDPETPVTILHNSEGVPASYSRQGFNG	180						
Qy	181	TFTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
Db	181	TFTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240						
Qy	241	EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300						

Db 241 EVVDLQWYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Qy 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360
Db 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFPRDGLVLRVLG 600
Qy 601 SGAFKGVVEGTAYGLRSQPMKVAVQMLKPTARSSEKQALMSELKIMTHLGPLHNI 660
Db 601 SGAFKGVVEGTAYGLRSQPMKVAVQMLKPTARSSEKQALMSELKIMTHLGPLHNI 660
Qy 661 LGACTKSGPIYIIITEYCFYGDVNLVHLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNLVHLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRLSDRPAKYKKSMMLDSEVKXN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRLSDRPAKYKKSMMLDSEVKXN 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Db 841 RDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Qy 901 VDSFTFNKIKSGYRMAKPDHATSEVYIEMVKCNWSEPEKRPSEFHLSEIVENLLPGQYKK 960
Db 901 VDSFTFNKIKSGYRMAKPDHATSEVYIEMVKCNWSEPEKRPSEFHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRRHSSQTSSESATETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRRHSSQTSSESATETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 3
US-08-460-490-4
; Sequence 4, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES

; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-490-4
Query Match 100.0%; Score 5652; DB 2; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSHPAFLVLGCLLTGSLILQSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGSLILQSLPSILPNENKVVQLNSFSRLRCFGESEVSWQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Qy 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPTLHNSGVPASYSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPTLHNSGVPASYSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKFKQTI PFNVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKFKQTI PFNVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
Qy 241 EVVDLQWYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Db 241 EVVDLQWYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Qy 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360
Db 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFPRDGLVLRVLG 600

Db 541 SLIVLVVWKQKPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFGKVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSLKMTHLGPLHNIVNL 660
Db 601 SGAFGKVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSLKMTHLGPLHNIVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMMDKQADTTQYVPMLEKVEVSKYSIDIQRLSYDRPASYYKKSMMLDSEVK 780
Db 721 VILSFENNGDYMMDKQADTTQYVPMLEKVEVSKYSIDIQRLSYDRPASYYKKSMMLDSEVK 780
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIHDSNVYVSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
Db 841 RDIHDSNVYVSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
QY 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFYHLSEIVENLLPGQYK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFYHLSEIVENLLPGQYK 960
QY 961 SYEKIHDLFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHDLFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
QY 1021 PLPDIDPVPEEEDLGKRRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 4
US-08-462-728-2
; Sequence 2, Application US/08462728
; Patent No. 6043211
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,728
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-728-2

Query Match 100.0%; Score 5652; DB 3; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVKVQLNSSPSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVKVQLNSSPSLRCFGESEVSWQYP 60
QY 61 MSEEESDVEIRNEENNSGLFVTIVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTIVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI 120
QY 121 VPDPDVAFVPLGMDTYLVIVVEDDDSAIIPCRTTDPETPTVLHNSEGVVPASYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVVEDDDSAIIPCRTTDPETPTVLHNSEGVVPASYDSRQGFNG 180
QY 181 TFTVGPYICEATVKGKFKQTIPFNVIYALKATSELDEMEALKTVYKSETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKFKQTIPFNVIYALKATSELDEMEALKTVYKSETIVVTCVFN 240
QY 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
Db 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300
QY 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISWLKNNLTNIENL 360
Db 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISWLKNNLTNIENL 360
QY 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGSTGGQTVRCTAEGTFLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTFLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
QY 541 SLIVLVVWKQKPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVWKQKPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFGKVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSLKMTHLGPLHNIVNL 660
Db 601 SGAFGKVVEGTAYGLRSQPMKVAVKMLKPTARSSEKQALMSLKMTHLGPLHNIVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNVYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMMDKQADTTQYVPMLEKVEVSKYSIDIQRLSYDRPASYYKKSMMLDSEVK 780
Db 721 VILSFENNGDYMMDKQADTTQYVPMLEKVEVSKYSIDIQRLSYDRPASYYKKSMMLDSEVK 780
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy 841 RDIMHDSNYVSKGSTFLPVKWNAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWNAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEYHLSSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEYHLSSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 5

US-08-461-917-2
; Sequence 2, Application US/08461917
; Patent No. 6372438
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-917-2

Query Match 100.0%; Score 5652; DB 3; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPILPNEKVVQNLSSFSRLRCFGESEVSWQYP 60
|||||

Db 1 MGTSHPAFLVGLCLLTGLSLILCQLSLPILPNEKVVQNLSSFSRLRCFGESEVSWQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYI 120
Qy 121 VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPETVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPETVTLHNSGVVPASYSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKFOITPFNVYALKATSELDLEMEALKTIVYKSGETIVVTCVFN 240
Db 181 TFTVGPYICEATVKGKFOITPFNVYALKATSELDLEMEALKTIVYKSGETIVVTCVFN 240
Qy 241 EVVDLQWTPGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db 241 EVVDLQWTPGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Qy 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNLTLIEN 360
Db 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNLTLIEN 360
Qy 361 TEITDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAETGPLDIEWMICKIKCNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAETGPLDIEWMICKIKCNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Qy 541 SLIVLVVWIKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
Db 541 SLIVLVVWIKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
Qy 601 SGAFKVVVEGTAYGLSRQPVKAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660
Db 601 SGAFKVVVEGTAYGLSRQPVKAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660
Qy 661 LGACTKSGPIYIITEYCFYGLVNYLHKNRDSEFLSHHPEKPKKELDIFGLNPADESTR 720
Db 661 LGACTKSGPIYIITEYCFYGLVNYLHKNRDSEFLSHHPEKPKKELDIFGLNPADESTR 720
Qy 721 VILSFENNGDYMDMKQADTTQVPMLEKEVSKYSIQRSLYDRPASYYKKSMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQVPMLEKEVSKYSIQRSLYDRPASYYKKSMLDSEVKN 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWNAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWNAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEYHLSSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSEYHLSSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 6
US-08-464-436-2
; Sequence 2, Application US/08464436
; Patent No. 6514723
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,436
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-436-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSRLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYVYNTQTEENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYVYNTQTEENELEGRHIYIY	120
Qy	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTVTLHNSGWPASYSRQGFNG	180
Db	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTVTLHNSGWPASYSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIENL	360

Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIENL	360
Qy	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWTILANNVSNITTEIHSRD	480
Db	421	VDDHGSTGGQTVRCTAEGTLPDIEWMICKDIKKCNNETSWTILANNVSNITTEIHSRD	480
Qy	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTILRSELTVAAAVLVLLVIVII	540
Db	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTILRSELTVAAAVLVLLVIVII	540
Qy	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPQVDSRWEPFRDGLVLRVLG	600
Db	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPQVDSRWEPFRDGLVLRVLG	600
Qy	601	SGAFKVVEGTAYGLRSQPVNKMVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL	660
Db	601	SGAFKVVEGTAYGLRSQPVNKMVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL	660
Qy	661	LGACTKSGPIYIIITEYCFYGDVLYLHKNRDSFSLSHHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTKSGPIYIIITEYCFYGDVLYLHKNRDSFSLSHHPEKPKKELDIFGLNPADESTRSY	720
Qy	721	VILSFENNGDYMCKQADTTQVPMLEKESKYSYDIQSLYDRPASYSKMSMLDSEVKN	780
Db	721	VILSFENNGDYMCKQADTTQVPMLEKESKYSYDIQSLYDRPASYSKMSMLDSEVKN	780
Qy	781	LILSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LILSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVNSYGILLWEIFSLGGTYPGMM	900
Db	841	RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVNSYGILLWEIFSLGGTYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKPSFYHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKPSFYHLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVSDNAYIGVYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVSDNAYIGVYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAETGSSSSTFKREDETIEDIDMDDDIGDS	1080
Db	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAETGSSSSTFKREDETIEDIDMDDDIGDS	1080
Qy	1081	SDLVEDSFL 1089	
Db	1081	SDLVEDSFL 1089	

RESULT 7
US-08-464-436-2
; Sequence 2, Application US/08464436
; Patent No. 6542022
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,436
FILING DATE: 05-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-267-2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-464-436-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60
QY 61 MSEEESDVEIRNEENNSGLFTVLEVSASAAHTGLTCVYNHTQTEENELEGRHIYIY 120
Db 61 MSEEESDVEIRNEENNSGLFTVLEVSASAAHTGLTCVYNHTQTEENELEGRHIYIY 120
QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYDSRQGFNG 180
QY 181 TFTVGPICEATVGKKFQTFIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TFTVGPICEATVGKKFQTFIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY 241 EVVDLQWTPGVEVGKGIITMLEEIKVPSIKLVYTLTVPEATVKSDGYECAARQATREVK 300
Db 241 EVVDLQWTPGVEVGKGIITMLEEIKVPSIKLVYTLTVPEATVKSDGYECAARQATREVK 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
QY 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGGSTGGQTVRCTAEGTPLDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAA VLVLLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAA VLVLLVIVII 540
QY 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
Db 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600

QY 601 SCAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHNLVNL 660
Db 601 SCAFKVVVEGTAYGLSRSPVMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHNLVNL 660
QY 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFSLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFSLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSIDIQSLYDRPASYYKKSMMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSIDIQSLYDRPASYYKKSMMLDSEVKN 780
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
Db 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPYPGMM 900
QY 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCWNSPEKRPSPFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCWNSPEKRPSPFYHLSEIVENLLPGQYKK 960
QY 961 SYEKIHLDFLKSDHPAVARNRVSDSNAYIGVYTKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARNRVSDSNAYIGVYTKNEEDKLDWEGGLDEQRLSADSGYII 1020
QY 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEYSGSSSTFIKREDETIEDIMDDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEYSGSSSTFIKREDETIEDIMDDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 8

US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. 6660488
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
; FILE REFERENCE: 14014.0266U2
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6660488e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60

Db	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENEKVQVQLNSSFSRLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120
Qy	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG	180
Db	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKGFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Db	181	TFTVGPYICEATVKGKGFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Qy	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Db	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Qy	301	EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIEN	360
Db	301	EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIEN	360
Qy	361	TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR	480
Db	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII	540
Qy	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Db	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Qy	601	SGAFKVVVEGTAYGLSRSQPVKMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV	660
Db	601	SGAFKVVVEGTAYGLSRSQPVKMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV	660
Qy	661	LGACTKSGPIYIIITEYCFYGDLVNLYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR	720
Db	661	LGACTKSGPIYIIITEYCFYGDLVNLYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR	720
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKERVSKYSDIQRSLYDRPASYYKKSMLDSEVK	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKERVSKYSDIQRSLYDRPASYYKKSMLDSEVK	780
Qy	781	LILSDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LILSDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL 1089	

Db	1081	SDLVEDSFL 1089	
RESULT 9			
US-09-866-510-2			
; Sequence 2, Application US/09866510			
; Patent No. 6667173			
; GENERAL INFORMATION:			
; APPLICANT: KAZLAUSKAS, ANDRIUS			
; APPLICANT: IKUNO, YASUSHI			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES			
; FILE REFERENCE: ERM-104.01			
; CURRENT APPLICATION NUMBER: US/09/866,510			
; CURRENT FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/250,747			
; PRIOR FILING DATE: 2000-12-01			
; PRIOR APPLICATION NUMBER: 60/289,103			
; PRIOR FILING DATE: 2001-05-07			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 2			
; LENGTH: 1089			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-866-510-2			
Query Match 100.0%; Score 5652; DB 4; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENEKVQVQLNSSFSRLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENEKVQVQLNSSFSRLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120
Db	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYI	120
Qy	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG	180
Db	121	VPDPVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYDSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKGFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Db	181	TFTVGPYICEATVKGKGFQTFPNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN	240
Qy	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Db	241	EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Qy	301	EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIEN	360
Db	301	EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIEN	360
Qy	361	TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR	480
Db	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII	540
Qy	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Db	541	SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Qy	601	SGAFKVVVEGTAYGLSRSQPVKMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV	660
Db	601	SGAFKVVVEGTAYGLSRSQPVKMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLV	660

Qy 661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDIORSLYDRPASYYKKSMMLDSEVK 780
Db 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDIORSLYDRPASYYKKSMMLDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 10
US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-90

Query Match 100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY 120
Qy 121 VPDPDVAFPVPLGMDTYLVIVEDDSDAIIPCRITDPETPVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPDVAFPVPLGMDTYLVIVEDDSDAIIPCRITDPETPVTLHNSGVVPASYSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240
Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240

Qy 241 EVVDLQWTPGEVKGKIGITMLBEIKVPSIKLVYTLTVPEATVKDGDYECARQATREV 300
Db 241 EVVDLQWTPGEVKGKIGITMLBEIKVPSIKLVYTLTVPEATVKDGDYECARQATREV 300
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVAYPPRISWLKNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVAYPPRISWLKNLTLIENL 360
Qy 361 TEITTDVEKIOEIRYRSKLLIRAKEEDSCHYTIIVAQNEHAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIOEIRYRSKLLIRAKEEDSCHYTIIVAQNEHAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGGSTGGQTVRCTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGGSTGGQTVRCTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Qy 541 SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMPQLPYDSRWEFFRDGLVLRVLG 600
Db 541 SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMPQLPYDSRWEFFRDGLVLRVLG 600
Qy 601 SGAFKVVVEGTAYGLSRSQPVKMAVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHNLVNL 660
Db 601 SGAFKVVVEGTAYGLSRSQPVKMAVAVKMLKPTARSSSEKQALMSELKIMTHLGPLHNLVNL 660
Qy 661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNVYLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDIORSLYDRPASYYKKSMMLDSEVK 780
Db 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDIORSLYDRPASYYKKSMMLDSEVK 780
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Qy 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Db 901 VDSFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYII 1020
Qy 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHRSSQTSEESAETGSSSSTFIKREDETIEDIDMDDIGIDS 1080
Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 11
US-09-949-016-6703
; Sequence 6703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

		PRIOR APPLICATION NUMBER: 60/241,755	
		PRIOR FILING DATE: 2000-10-20	
		PRIOR APPLICATION NUMBER: 60/237,768	
		PRIOR FILING DATE: 2000-10-03	
		PRIOR APPLICATION NUMBER: 60/231,498	
		PRIOR FILING DATE: 2000-09-08	
		NUMBER OF SEQ ID NOS: 207012	
		SOFTWARE: FastSeq for Windows Version 4.0	
		SEQ ID NO 6703	
		LENGTH: 1089	
		TYPE: PRT	
		ORGANISM: Human	
		US-09-949-016-6703	
		Query Match 100.0%; Score 5652; DB 4; Length 1089;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNSGLFVTLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI	120
Db	61	MSEESSDVEIRNEENNSGLFVTLEVSSASAAHTGLTYCYNHTQTENELEGRHIYI	120
Qy	121	VPDPDAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVPASYDSRQFNG	180
Db	121	VPDPDAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPTVLHNSGVPASYDSRQFNG	180
Qy	181	TFTVGPYICEATVGKKFQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN	240
Db	181	TFTVGPYICEATVGKKFQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCVFN	240
Qy	241	EVVDLQWYTPGEVKGKIGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Db	241	EVVDLQWYTPGEVKGKIGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLIEN	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPVPPRISWLKNNLTLIEN	360
Qy	361	TEITDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVNIITEIHSRD	480
Db	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVNIITEIHSRD	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLLVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLLVII	540
Qy	541	SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVGRVLG	600
Db	541	SLIVLVIIWKQPRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVGRVLG	600
Qy	601	SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNI	660
Db	601	SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNI	660
Qy	661	LGACTKSGPIYIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR	720
Db	661	LGACTKSGPIYIITEYCFYGLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR	720
Qy	721	VILSPENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQSLYDRPASVKKKMLDSEVK	780
Db	721	VILSPENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQSLYDRPASVKKKMLDSEVK	780
Qy	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGL	840
Db	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGL	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTILSDVWSYGILLWEIFSLGGTYPGMM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTILSDVWSYGILLWEIFSLGGTYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVSDNAYIGVYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVSDNAYIGVYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEIETGSSSSTFIKREDETIEDIMDDIGIDS	1080
Db	1021	PLPDIDPVPEEEDLGKRNHRSSQTSEESAIEIETGSSSSTFIKREDETIEDIMDDIGIDS	1080
Qy	1081	SDLVEDSFL 1089	
Db	1081	SDLVEDSFL 1089	
RESULT 12			
PCT-US92-00730-4			
; Sequence 4, Application PC/TUS9200730			
; GENERAL INFORMATION:			
; APPLICANT: Wolf, David			
; APPLICANT: Tomlinson, James E.			
; APPLICANT: Fretto, Larry J.			
; APPLICANT: Giese, Neill A.			
; APPLICANT: Escobedo, Jaime A.			
; APPLICANT: Williams, Lewis T.			
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN			
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES			
; NUMBER OF SEQUENCES: 23			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: TOWNSEND and TOWNSEND			
; STREET: Steuart Street Tower, 20th Floor \ One Market			
; STREET: Plaza			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: US			
; ZIP: 94105			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: PCT/US92/00730			
; FILING DATE: 19920128			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Ching, Edwin P.			
; REGISTRATION NUMBER: 34,090			
; REFERENCE/DOCKET NUMBER: 12418-14			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 326-2400			
; TELEFAX: (415) 326-2422			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1089 amino acids			
; TYPE: AMINO ACID			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
PCT-US92-00730-4			
Query Match 100.0%; Score 5652; DB 5; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP	60

Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60

Qy 61 MSEEESDVVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Db 61 MSEEESDVVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Qy 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYSRQGFNG 180

Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYSRQGFNG 180

Qy 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240

Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240

Qy 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

Db 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNLTLIENL 360

Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNLTLIENL 360

Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Db 421 VDDHGGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Db 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Qy 541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600

Db 541 SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600

Qy 601 SGAFGKVEGTAYGLRSQPVMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI VNL 660

Db 601 SGAFGKVEGTAYGLRSQPVMKVAVKMLKPTARSSEKQALMSELKINTHLGPHLNI VNL 660

Qy 661 LGACTKSGPIYIIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720

Db 661 LGACTKSGPIYIIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720

Qy 721 VILSPENNGDYMDMKQADTTQYVPMLEKESKYSDIQRSLYDRPASYYKKSMLDSEVK 780

Db 721 VILSPENNGDYMDMKQADTTQYVPMLEKESKYSDIQRSLYDRPASYYKKSMLDSEVK 780

Qy 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPCNM 900

Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPCNM 900

Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK 960

Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK 960

Qy 961 SYEKIHLDFLKS DHPAARMRVDS DNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020

Db 961 SYEKIHLDFLKS DHPAARMRVDS DNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020

Qy 1021 PLPDI DPVPEEEDLGKRNHSSQTSEESA IETGSSSSTFIKREDETIEDIMMDDIGIDS 1080

Db 1021 PLPDI DPVPEEEDLGKRNHSSQTSEESA IETGSSSSTFIKREDETIEDIMMDDIGIDS 1080

Qy 1081 SDLVEDSFL 1089

Db 1081 SDLVEDSFL 1089

RESULT 13

PCT-US92-00862-4

; Sequence 4, Application PC/TUS9200862

; GENERAL INFORMATION:

; APPLICANT: Williams, Lewis T.

; APPLICANT: Escobedo, Jaime A.

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND

; STREET: Steuart Street Tower, 20th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00862

; FILING DATE: 19920131

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/151,141

; FILING DATE: 02-FEB-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/309,322

; FILING DATE: 10-FEB-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: 2307U-267-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1089 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00862-4

Query Match 100.0%; Score 5652; DB 5; Length 1089;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60

Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSRLRCFGESEVSWQYP 60

Qy 61 MSEEESDVVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Db 61 MSEEESDVVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Qy 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYSRQGFNG 180

Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRTTDPETPVTLHNSGVVPASYSRQGFNG 180

Qy 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240

Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240

Qy 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

Db 241 EVVDLQWTPGGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNLTLIENL 360

Db 301 EMKKVTISVHEKGFIEIKPTFSQLAEVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
QY 361 TEITTDVEKIQEIRYRSKLIKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLIKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLVIVII 540
QY 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
Db 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
QY 601 SGAFGKVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
Db 601 SGAFGKVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
QY 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
QY 901 VDSIFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Db 901 VDSIFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
QY 961 SYEKTHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020
Db 961 SYEKTHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020
QY 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
Db 1021 PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTGSSSSTFIKREDETIEDIMMDDIGIDS 1080
QY 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

RESULT 14

US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866, 510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250, 747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289, 103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10

; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-10

Query Match 99.9%; Score 5649; DB 4; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQNLNSSFSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVQNLNSSFSLRCFGESEVSWQYP 60
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY 120
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY 120
QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTETPVTLHNSEGVPASYSRQGFNG 180
Db 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTETPVTLHNSEGVPASYSRQGFNG 180
QY 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240
Db 181 TFTVGPYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTVYKSGETIVVTCAVFNN 240
QY 241 EVVDLQWTPGVEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Db 241 EVVDLQWTPGVEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLAEVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLAEVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
QY 361 TEITTDVEKIQEIRYRSKLIKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLIKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLVIVII 540
QY 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
Db 541 SLIVLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600
QY 601 SGAFGKVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
Db 601 SGAFGKVEGTAYGLSRQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIIVNL 660
QY 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
Db 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMLDSEVKN 780
QY 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
QY 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
Db 841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTYPGMM 900
QY 901 VDSIFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSEFYHLSEIVENLLPGQYKK 960
Db 901 VDSIFYNKIKSGYRMAKPDHATSEVYEIMVKCNSEPEKRPSEFYHLSEIVENLLPGQYKK 960

Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020

Qy 1021 PLPDIDVPVEEEDLGKRNHRSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDVPVEEEDLGKRNHRSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080

Qy 1081 SOLVEDSFL 1089
Db 1081 SOLVEDSFL 1089

RESULT 15
US-08-180-195-36
; Sequence 36, Application US/08180195
; Patent No. 5567584
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,195
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,510
; FILING DATE:
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-180-195-36

Query Match 99.9%; Score 5648; DB 1; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60

Qy 61 MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120
Db 61 MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Qy 121 VPDPDAFVPLGMTDYLVIVEDDSAIIPCRTTDPETPVLHNSGVVPASYSRQGFNG 180
Db 121 VPDPDAFVPLGMTDYLVIVEDDSAIIPCRTTDPETPVLHNSGVVPASYSRQGFNG 180

Qy 181 TFTVGPIYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTIVYKSGETIVVTCVAFNN 240
Db 181 TFTVGPIYICEATVKGKFKQTIPFNVYALKATSELDEMEALKTIVYKSGETIVVTCVAFNN 240

Qy 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Db 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300

Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPRISWLKNNLTLIENL 360

Qy 361 TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKOIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKOIKKCNNETSWTILANNVSNIIITEIHSRD 480

Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLVIVII 540

Qy 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600
Db 541 SLIVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRDGLVLRVLG 600

Qy 601 SGAFKGVVEGTAYGLSRSQPVNKAVMKLPKTARSSEKQALMSELKIMTHLGPLHLNIVNL 660
Db 601 SGAFKGVVEGTAYGLSRSQPVNKAVMKLPKTARSSEKQALMSELKIMTHLGPLHLNIVNL 660

Qy 661 LGACTKSGPIYIITEYCFYGDVNLVYLNKRDLSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVYLNKRDLSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy 721 VILSFENNGDYMDMKQADTTQVPMLEKEVSKYSIDIORSLYDRPASYYKKSMULDSEVK 780
Db 721 VILSFENNGDYMDMKQADTTQVPMLEKEVSKYSIDIORSLYDRPASYYKKSMULDSEVK 780

Qy 781 LLSDDNSEGLTLDDLSTFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDDLSTFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy 841 RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db 841 RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKRPSPFYHLSEIVENLLPGQYKK 960
Db 901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKRPSPFYHLSEIVENLLPGQYKK 960

Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARMRVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020

Qy 1021 PLPDIDVPVEEEDLGKRNHRSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080
Db 1021 PLPDIDVPVEEEDLGKRNHRSSQTSESAIETGSSSSTFIKREDETIEDIDMDDDIGIDS 1080

Qy 1081 SDLVEDSFL 1089
Db 1081 SDLVEDSFL 1089

Search completed: March 11, 2005, 07:50:27
Job time : 36.7522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:07:56 ; Search time 33.7367 Seconds
(without alignments)
3105.821 Million cell updates/sec

Title: US-10-027-400-2
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5652	100.0	1089	1 PFHUGA	platelet-derived g
2	5190.5	91.8	1088	1 PFRTGA	platelet-derived g
3	5177	91.6	1089	1 S33727	platelet-derived g
4	4246	75.1	1087	2 I51552	platelet-derived g
5	2354.5	41.7	1106	1 PFHUGB	platelet-derived g
6	2336.5	41.3	1098	1 PFMSRB	platelet-derived g
7	2182.5	38.6	1048	2 T30815	platelet-derived g
8	1914.5	33.9	457	2 S44269	platelet-derived g
9	1481.5	26.2	977	2 I45877	protein-tyrosine k
10	1461.5	25.9	960	1 JN0677	protein-tyrosine k
11	1458	25.8	978	1 A49814	protein-tyrosine k
12	1454.5	25.7	976	1 TVHUKT	protein-tyrosine k
13	1446.5	25.6	975	1 TVMSKT	protein-tyrosine k
14	1416.5	25.1	954	2 I51703	c-kit-related kina
15	1412.5	25.0	980	1 TVCTMD	macrophage colony-
16	1400.5	24.8	941	1 TVMVMD	protein-tyrosine k
17	1395	24.7	975	2 T30816	macrophage colony-
18	1352.5	23.9	978	2 S16385	macrophage colony-
19	1346.5	23.8	972	1 TVHUMD	macrophage colony-
20	1344	23.8	976	1 TVMSMD	macrophage colony-
21	1287	22.8	1338	2 S09982	protein-tyrosine k
22	1280	22.6	1333	2 I78875	receptor tyrosine
23	1278	22.6	1336	2 I60598	Fit-1 tyrosine kin
24	1231.5	21.8	1330	2 S49010	embryonic receptor
25	1226	21.7	1348	2 S51656	vascular endotheli
26	1206.5	21.3	1356	2 JC1402	protein-tyrosine k
27	1198.5	21.2	1379	2 JC4954	vascular endotheli
28	1164.5	20.6	1000	2 S18827	Flt3 protein - mou
29	1163.5	20.6	1298	2 A48999	protein-tyrosine k

30	1152.5	20.4	992	2 A39931	protein-tyrosine k
31	1152.5	20.4	1363	2 I58375	protein-tyrosine k
32	1152	20.4	1367	2 A41228	protein-tyrosine k
33	1151	20.4	993	2 A36873	protein-tyrosine k
34	1067	18.9	790	1 FOMVHZ	gag-kit polyprotei
35	863	15.3	819	1 TVCHFG	fibroblast growth
36	859.5	15.2	822	1 TVHUPG	fibroblast growth
37	855	15.1	822	2 S29840	fibroblast growth
38	854	15.1	812	1 A36477	fibroblast growth
39	852.5	15.1	822	2 I49289	fibroblast growth
40	849.5	15.0	822	1 TVMSFG	fibroblast growth
41	846	15.0	814	1 A39752	fibroblast growth
42	843.5	14.9	832	2 JH0393	fibroblast growth
43	841.5	14.9	816	2 A49151	fibroblast growth
44	841	14.9	797	2 S38579	fibroblast growth
45	833.5	14.7	821	1 TVHUF2	fibroblast growth

ALIGNMENTS

RESULT 1

PFHUGA

platelet-derived growth factor receptor alpha precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A40162; A32941

R:Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle, W.; Kraus, M.; Pierce, J Science 243, 800-804, 1989

A:Title: Isolation of a novel receptor cDNA establishes the existence of two PDGF recepto A:Reference number: A40162; MUID:89130149; PMID:2536956

A:Accession: A40162

A:Molecule type: mRNA

A:Residues: 1-1089 <MATS>

A:Cross-references: UNIPROT:P16234; GB:M21574; NID:g189733; PIDN:AAA96715.1; PID:g189734 R:Claesson-Welsh, L.; Eriksson, A.; Westermarck, B.; Heldin, C.H.

Proc. Natl. Acad. Sci. U.S.A. 86, 4917-4921, 1989

A:Title: cDNA cloning and expression of the human A-type platelet-derived growth factor A:Reference number: A32941; MUID:89296915; PMID:2544881

A:Accession: A32941

A:Molecule type: mRNA

A:Residues: 1-1089 <CLA>

A:Cross-references: GB:M22734; NID:g189725; PIDN:AAA60048.1; PID:g189726

C:Comment: The extracellular domain is predicted to include five immunoglobulin-like doma C:Genetics:

A:Gene: GDB:PDGFRA

A:Map position: 4q11-4q12

A:Cross-references: GDB:120267; OMIM:173490

C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology; C:Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phosph

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1089/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>

F:25-524/Domain: extracellular #status predicted <EXT>

F:42-102/Domain: immunoglobulin homology <IMM1>

F:143-191/Domain: immunoglobulin homology <IMM2>

F:228-292/Domain: immunoglobulin homology <IMM3>

F:428-503/Domain: immunoglobulin homology <IMM4>

F:525-548/Domain: transmembrane #status predicted <TMM>

F:549-1089/Domain: intracellular #status predicted <INT>

F:591-957/Domain: protein kinase homology <KIN>

F:599-607/Region: protein kinase ATP-binding motif

F:42,76,103,179,353,458,468/Binding site: carbohydrate (Asn) (covalent) #status predi F:49-100,150-189,235-290,435-501/Disulfide bonds: #status predicted

F:627/Active site: Lys #status predicted

F:849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 100.0%; Score 5652; DB 1; Length 1089;

Best Local Similarity 100.0%; Pred. No. 3.3e-238;

Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFILRCFGESEVSWQYP 60
|||||

Db	1	MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVLNSSFSLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEENNGLFVTLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEENNGLFVTLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY	120
Qy	121	VPDPDAFVPLGMTDYLIVVEDDDSAIIPCRRTDPETPVTLHNSGWWPASYDSRQGFNG	180
Db	121	VPDPDAFVPLGMTDYLIVVEDDDSAIIPCRRTDPETPVTLHNSGWWPASYDSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKKFQTIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICEATVKGKKFQTIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWYTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLQWYTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360
Qy	361	TEITTDVEKIQEIYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHHGSTGQTVRCTAEGTPLPDIEMWICKDIKKCNNETSWTILANNVSNIIITEIHSRD	480
Db	421	VDDHHGSTGQTVRCTAEGTPLPDIEMWICKDIKKCNNETSWTILANNVSNIIITEIHSRD	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLLVIVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLLVIVII	540
Qy	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Db	541	SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLRVLG	600
Qy	601	SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNI	660
Db	601	SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNI	660
Qy	661	LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKKEVSKYSDIQRSLYDRPASYYKKSMULDSEVK	780
Qy	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYIEMVKWNSEPEKRPSEFYLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYIEMVKWNSEPEKRPSEFYLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII	1020
Qy	1021	PLPDIDPVEEEDLGKRRNRHSSQTSESALETGSSSSTFIKREDETIEDIDMDDDIGIDS	1080
Db	1021	PLPDIDPVEEEDLGKRRNRHSSQTSESALETGSSSSTFIKREDETIEDIDMDDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089

RESULT 2

PFRTGA

platelet-derived growth factor receptor alpha precursor - rat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C;Accession: A34710; S33767; S25100

R;Lee, K.H.; Bowen-Pope, D.F.; Reed, R.R.

Mol. Cell. Biol. 10, 2237-2246, 1990

A;Title: Isolation and characterization of the alpha platelet-derived growth factor recei

A;Reference number: A34710; MUID:90220609; PMID:2157969

A;Accession: A34710

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1088 <LEE>

A;Cross-references: UNIPROT:P20786; GB:M63837; NID:g202929; PIDN:AAA40743.1; PID:g202930

A;Note: in the authors' translation an additional residue, Val, is shown after position 8

R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Biochim. Biophys. Acta 1173, 294-302, 1993

A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and recei

A;Reference number: S33764; MUID:93305723; PMID:8318539

A;Accession: S33767

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 33-149,'R',151-518,'T',520-523 <HER1>

A;Cross-references: EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID:g56864

A;Experimental source: strain Sprague Dawley

R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Submitted to the EMBL Data Library, July 1992

A;Description: Cross-species conservation in sequence and function of PDGF ligands and r

A;Reference number: S25096

A;Accession: S25100

A;Molecule type: mRNA

A;Residues: 33-149,'R',151-518,'T',520-523 <HER2>

A;Cross-references: EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID:g56864

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; glycoprotein; heterodimer; homodimer; phosphoprotei

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-1088/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>

F;24-523/Domain: extracellular #status predicted <EXT>

F;41-101/Domain: immunoglobulin homology <IMM1>

F;142-190/Domain: immunoglobulin homology <IMM2>

F;227-291/Domain: immunoglobulin homology <IMM3>

F;427-502/Domain: immunoglobulin homology <IMM4>

F;524-547/Domain: transmembrane #status predicted <TMM>

F;548-1088/Domain: intracellular #status predicted <INT>

F;590-956/Domain: protein kinase homology <KIN>

F;598-606/Region: protein kinase ATP-binding motif

F;48-99,149-188,234-289,434-500/Disulfide bonds: #status predicted

F;75,76,88,102,178,352,358,457,467/Binding site: carbohydate (Asn) (covalent) #status p

F;626/Active site: lys #status predicted

F;848/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 91.8%; Score 5190.5; DB 1; Length 1088;

Best Local Similarity 90.9%; Pred. No. 3.6e-218;

Matches 990; Conservative 55; Mismatches 43; Indels 1; Gaps 1;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVLNSSFSLRCFGESEVSWQYP 60

Db 1 MGTSQ-AFLVLSCLLTGPSLLVCQLLPSILPNENEKIVPLSSSFSLRCFGESEVSWQHP 59

Qy 61 MSEESSDVEIRNEENNGLFVTLEVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIY 120

Db 60 MSEEDDPNVEIRTEENNSSLFVTLEVNVNASAAHTGWYTCYNNHTQTEESEIEGRHIYIY 119

Qy 121 VPDPDAFVPLGMTDYLIVVEDDDSAIIPCRRTDPETPVTLHNSGWWPASYDSRQGFNG 180

Db 120 VPDPDAFVPLGMTDSLIVVEEDDSAIIPCLTTDPDTEVTLHNNRLVPASYDSRQGFNG 179

Qy 181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Db 181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Db 180 TFSVGPYICEATVRGRTEKTSSENVYALKATSELNLEMDTRQTVYKAGETIVVTCVFN 239

Qy 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300

Db 240 EVVDLQWTPYGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGDYECARQATKEV 299

Qy 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVGHFVVEVRAVPPPRISWLKNNLTLIENL 360

Db 300 EMKTIVTSVHEKGFVQIRPTFGHLETVNLHQVREFVVEVQAYPTPRISWLKNNLTLIENL 359

Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Db 360 TEITTDVQRSQETRYQSKLLIRAKEEDSGHYTIIIVQNDDMKSYTFELSTLVPASILEL 419

Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Db 420 VDDHSGGGQTVRCTAEGTPLPNIEWMICKDIKKCNNDTSWTVLASVNSNIITEFHQRG 479

Qy 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Db 480 RSTVEGRVSAKVEETIAVRCLAKNDLGIGNRELKLVAPLSRSELTVAAAVLVLVIVIV 539

Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600

Db 540 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRILG 599

Qy 601 SGAFGKVVEGTAYGLRSQPVKMAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Db 600 SGAFGKVVEGTAYGLRSQPVKMAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 659

Qy 661 LGACTKSGPIYIIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db 660 LGACTKSGPIYIIITEYCFYGDVNLVHLKNRDSFMSRHPEKPKKOLDIFGLNPADESTRSY 719

Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSIDIQRSLYDRPASYYKKSMLDSEVK 780

Db 720 VILSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSIDIQRSLYDRPASYYKKSMLDSEAK 779

Qy 781 LLSDDNSEGLTLDDLSTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db 780 LLSDDNSEGLTLDDLSTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 839

Qy 841 RDIMHDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGWM 900

Db 840 RDIMHDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYPGWM 899

Qy 901 VDSFTFNKIKSGYRMAKPDHATSEVVEIMVKNSEPEKRPSEVHLSEIVENLLPGQYKK 960

Db 900 VDSFTFNKIKSGYRMAKPDHATSEVVEIMVQCNSEPEKRPSEVHLSEIVENLLPGQYKK 959

Qy 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db 960 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1019

Qy 1021 PLPDIDPVPEEEDLGKRRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1080

Db 1020 PLPDIDPVPEEEDLGKRRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1079

Qy 1081 SDLVEDSFL 1089

Db 1080 SDLVEDSFL 1088

RESULT 3

S33727

platelet-derived growth factor receptor alpha precursor - mouse

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I57511; S33727

R;Stiles, C.D.; Wang, C.

Mol. Cell. Biol. 10, 6781-6784, 1990

A;Title: Retinoic acid promotes transcription of the platelet-derived growth factor alph

A;Reference number: I57511; MUID:91061789; PMID:2174116

A;Accession: I57511

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1089 <RES>

A;Cross-references: UNIPROT:P26618; GB:M57683; NID:g199783; PIDN:AAA39733.1; PID:g199784

C;Genetics:

A;Gene: PDGF-alpha-R

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transmembrane

F;1-23/Domain: signal sequence #status predicted <SIG>

F;228-292/Domain: immunoglobulin homology <IMM>

F;591-957/Domain: protein kinase homology <KIN>

F;599-607/Region: protein kinase ATP-binding motif

F;42,76,89,103,179,353,359,458,468,506/Binding site: carbohydrate (Asn) (covalent) #stat

Query Match 91.6%; Score 5177; DB 1; Length 1089;

Best Local Similarity 91.0%; Pred. No. 1.4e-217;

Matches 991; Conservative 50; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60

Db 1 MGTSHQVFLVLSCLLTGPGLIQCQLLLPSILPNENKIVQLNSSFSLRCVGESEVSWQHP 60

Qy 61 MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCNHTQTENELEGRHIYIY 120

Db 61 MSEEDPNVEIRSEENNSGLFVTVLEVWNASAAHTGWYTCYNHTQTDESEIEGRHIYIY 120

Qy 121 VPDPDAFVPLGMDTVLVIIBEDDDSAIIPCRITDPETVTLHNSGWWPASYDSRQGFNG 180

Db 121 VPDPDAFVPLGMDTVLVIIBEDDDSAIIPCRITDPETVTLHNNGRLLVPASYDSRQGFNG 180

Qy 181 TFTVGPYICEATVKGKKFQITIPNVYALKATSELDEMEALKTVYKSGETIVVTCVFN 240

Db 181 TFSVGPYICEAAVKGRTEKTSFAPNVYALKATSELNLEMDARQTVYKAGETIVVTCVFN 240

Qy 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREV 300

Db 241 EVVDLQWTPYGGVRNKGITMLEEIKLPSIKVYTLTVPKATVKDSGEYECARQATKEV 300

Qy 301 EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVGHFVVEVRAVPPPRISWLKNNLTLIENL 360

Db 301 EMKKTIVSVHEKGFIEIPTFSQLEPVLNHEVREFVVEVQAYPTPRISWLKNNLTLIENL 360

Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

Db 361 TEITTDVQRSQETRYQSKLLIRAKEEDSGHYTIIIVQNEDDVKSYTFELSTLVPASILD 420

Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480

Db 421 VDDHSGGGQTVRCTAEEGPEIDWMICKHIKKCNNDTSWTVLASVNSNIITELPRRG 480

Qy 481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540

Db 481 RSTVEGRVSAKVEETIAVRCLAKNLLSVVARELKLVAPTLRSELTVAEAVLVLVIVIV 540

Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLG 600

Db 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRILG 600

Qy 601 SGAFGKVVEGTAYGLRSQPVKMAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Db 601 SGAFGKVVEGTAYGLRSQPVKMAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNL 660

Qy 661 LGACTKSGPIYIIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db 661 LGACTKSGPIYIIITEYCFYGDVNLVHLKNRDSFMSQHPEKPKKOLDIFGLNPADESTRSY 720

Qy 721 VILSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSIDIQRSLYDRPASYYKKSMLDSEVK 780

Db 721 VILSFENNGDYMDMKQDDTTQYVPMLEKVEVSKYSIDIQRSLYDRPASYYKKSMLDSEVK 780

Qy 781 LLSDDNSEGLTLDDLSTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db	781	LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Db	841	RDIMHDSNDVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKCNSEPEKRPSPFYHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVQCNWSDPEKRPSPFYHLSEILENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVITYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVITYKNEEDKLDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDVPPEEEDLGKRNHRSSQTSESAIETGSSSSSTFIKREDETIEDIDMDDDIGIDS	1080
Db	1021	PLPDIDVPPEEEDLGKRNHRSSQTSESAIETGSSSSSTFIKREDETIEDIDMDDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089
RESULT 4			
I51552			
platelet-derived growth factor A receptor - African clawed frog			
C;Species: Xenopus laevis (African clawed frog)			
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004			
C;Accession: I51552			
R;Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.			
Dev. Genet. 14, 185-193, 1993			
A;Title: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem			
ion.			
A;Reference number: I51552; MUID:93365089; PMID:8358864			
A;Accession: I51552			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: mRNA			
A;Residues: 1-1087 <JON>			
A;Cross-references: UNIPROT:P26619; GB:M80798; NID:G214652; PIDN:AAA49929.1; PID:G214653			
C;Genetics:			
A;Gene: PDGFAR			
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;			
C;Keywords: ATP; growth factor receptor			
F;43-103/Domain: immunoglobulin homology <IMM>			
F;593-957/Domain: protein kinase homology <KIN>			
F;601-609/Region: protein kinase ATP-binding motif			
Query Match 75.1%; Score 4246; DB 2; Length 1087;			
Best Local Similarity 75.6%; Pred. No. 3.8e-177;			
Matches 821; Conservative 104; Mismatches 153; Indels 8; Gaps 6;			
Qy	7	AFLVLGCLL-TGLSLILCOLSLPSILPNENEKVVQLNSSFSIRCFGESEVSWQYPMSEEE	65
Db	7	ASLILGCLLIIGPWAILAENPLPTIPDPKDELVQALHSSFTLKCTGESEVSWQNPNSNPE	66
Qy	66	SSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYYNHTQTENELEGRHIYIYVDPDP	125
Db	67	KQNVVIRSEENNSGLFVSVILEVSDASAFDTGLTYCYHNHTQTESEIEGTDIYIYVDPDN	126
Qy	126	VAFVPLGMDYLVIVEDDDSAIIPCRTPDPETPTVLHNSG--VVPASYSRQGFNGTFT	183
Db	127	VPFAPPGLFDHIIVVEEDESALVPCRTDPSSEVTLKNIESSRTVFAFYDSKQGFAGNFP	186
Qy	184	VGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVTVCAFNNEVV	243
Db	187	PGSYICETTSNKWVYQTEPYILQTWKATHNISVEMEAPKTMFRAGETIAIDCIVLDNEVV	246
Qy	244	DLQWTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVKEMK	303
Db	247	DLKWTPGKQRGVGIRNVEESKVPYQRLVYTLTLANATTEDSGEYECAVIHATLDNRVVK	306
Qy	304	KVTISVHEKGFIEIKPTFSQLEAVNLHVEVKHFVVEVRAYPPPRISWLKKNLTLIENLTEI	363

Db	307	KTNITVHEKGFIDLEPMFGSEEFANLHEVKSFIYNLHAYTPGLFWLKDNRTLSENLTEI	366
Qy	364	TTDVEKIQEIRYRSKLLIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDD	423
Db	367	TTTSIVTTKETRFQSKLLIRAKBEDSGLYTLVAQNDRKTSYSFIQIKVPALILELVDK	426
Qy	424	HHGSTGGQTVRCTAEGTPLPDIEWMICDKIKKCNNETSWTILANNVSNIIITEIHSRDRST	483
Db	427	HHGASGEQTVGCLAKGMPVPDVEWLVCCKDIKRCNNDTLWSILATNGSEISMETH-QDDEQ	485
Qy	484	VEGRVTEFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLI	543
Db	486	IESQVTFKKIETMAIRCIAKNELGVVARELKLVAPTLRSELTVAAAVLVLLVIVIISLI	545
Qy	544	VLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDPMQLPYDSRWEFFPRDGLVLRVLGSGA	603
Db	546	VLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDPMQLPYDSRWEFFPRDGLVLRVLGSGA	605
Qy	604	FGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGA	663
Db	606	FGKVVEGAAAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGAHLNIVNLLGA	665
Qy	664	CTKSGPIYIIITEYCFYGDLYNLYLHKNRDSFLSHHPEKPKBELDIFGLNPADESTRSYVIL	723
Db	666	CTKSGPIYIIITEYCFYGDLYNLYLHKNRDNFQSRHPEKPKKDLDFGLNPADESTRSYVIL	725
Qy	724	SFENNGDYMDMKQADTTQYVPMLEKESKYSIDIQRSLYDRPASYYKKSMLDSEVKNLLS	783
Db	726	SFENNGDYMDMKQADTMQYVPMLEMKESKYSIDIQRSLYDRPASYYKKPL--SEVKNILS	783
Qy	784	DDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDI	843
Db	784	DDGFEGLTVDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAHGKIVKICDFGLARDI	843
Qy	844	MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDS	903
Db	844	MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSFGILLWEIFSLGGTPYPGMIVDS	903
Qy	904	TFYNKIKSGYRMAKPDHATSEVVEIMVKCNSEPEKRPSPFYHLSEIVENLLPGQYKKSVE	963
Db	904	TFYNKIKSGYRMAKPDHATHEVYDIMVKCNSEPEKRPSPRHLSDIVESLLPMEYKRCVE	963
Qy	964	KIHLDFLKSDHPAVARMRVDSDNAYIGVITYKNEEDKLDWEGGLDEQRLSADSGYIILP	1023
Db	964	TVLHDFLKSDHPAVTRMRSDSNSYIGVITYKNEH-KMKDRESGFDEQRLSADSGYIILP	1022
Qy	1024	DIDVPPEEEDLGKRNHRSSQTSESAIETGSSSSSTFIKREDETIEDIDMDDDIGIDSDL	1083
Db	1023	DIDPVSEDES-GKRNHRSSQTSESAIETGSSSSSTFIKRDDDETIEDIDMDDDIGIDSDL	1081
Qy	1084	VEDSFL	1089
Db	1082	VEDSFL	1087
RESULT 5			
PFHUGB			
platelet-derived growth factor receptor beta precursor - human			
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)			
C;Species: Homo sapiens (man)			
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004			
C;Accession: A28206; A31195; A38268; A31925; B31925; C31925			
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.; I			
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988			
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth fa			
A;Reference number: A28206; MUID:88217915; PMID:2835772			
A;Accession: A28206			
A;Molecule type: mRNA			
A;Residues: 1-1106 <GRO>			
A;Cross-references: UNIPROT:P09619; GB:J03278; NID:g189731; PIDN:AAA60049.1; PID:g189732			
R;Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet			
Mol. Cell. Biol. 8, 3476-3486, 1988			

Nature 323, 226-232, 1986
A;Title: Structure of the receptor for platelet-derived growth factor helps define a fam
A;Reference number: A25742; MUID:87014762; PMID:3020426
A;Accession: A25742
A;Molecule type: mRNA
A;Residues: 1-1098 <YAR>
A;Cross-references: UNIPROT:P05622; EMBL:X04367; NID:G53618; PIDN:CAA27882.1; PID:G53619
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C;Comment: The purified receptor was found be ubiquitinated.
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-1098/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
F;32-530/Domain: extracellular #status predicted <EXT>
F;46-101/Domain: immunoglobulin homology <IMM1>
F;141-191/Domain: immunoglobulin homology <IMM2>
F;227-292/Domain: immunoglobulin homology <IMM3>
F;428-509/Domain: immunoglobulin homology <IMM4>
F;531-554/Domain: transmembrane #status predicted <TM>
F;555-1098/Domain: intracellular #status predicted <INT>
F;597-964/Domain: protein kinase homology <KIN>
F;605-613/Region: protein kinase ATP-binding motif
F;44,88,102,214,291,306,353,370,444,467,478/Binding site: carbohydrate (Asn) (covalent)
F;53-99,148-189,234-290,435-507/Disulfide bonds: #status predicted
F;633/Active site: Lys #status predicted
F;856/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 41.3%; Score 2336.5; DB 1; Length 1098;
Best Local Similarity 44.1%; Pred. No. 3.3e-94;
Matches 498; Conservative 192; Mismatches 356; Indels 83; Gaps 21;

QY 6 PAFLVLG-CLLTGLSLILCQLSLPSIL-PNENEKVQVQLNSSFSRLRCFGESEVSWQYPMSE 63
Db 8 PALVLRGQLLSVLWLLGPQTSRGLVITPPGPEFVLNISTFVLTCGSAVMW----- 61

QY 64 EESSDVEIRNEE-NNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIYVP 122
Db 62 EQMSQVPWQBEAAMNQDGTFFSSVLTLTNVTGGDTGEYFCVYNNSLGPELS-ERKRIYIFVP 120

QY 123 DPDAFVPLGMDYLVIVEDDDSAIIPCRTTDPETPTVLHNSEGVVP--ASYDSRQGFNG 180
Db 121 DPTMGFLPMDSIEDLFIFTVDVTETTPCRVTDPPQLEVTLHKVKVDIPLHVPYDHQRGFTG 180

QY 181 TFTVGPYICBATVKGKFKQTIPTFNVVVALKATSELDLEMEALKTVYKSGETIVVTCVAVFNN 240
Db 181 TFEDKTYICKTIGDREVDSDTYVYVSLQVSS-INVSNAVQTVVRQGESITIRCIVMGN 239

QY 241 EVVDLQWTFGEVKGKGITMLEE--IKVPSIKLVYTLTVPEATVKDSGDYECARQATRE 298
Db 240 DVVNFQWTFYPRMKSGRLVEPVTDYLFQVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

QY 299 VKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLE 358
Db 299 HGDEKAINISVIENGYVRLLETGLGDVEIAELHRSRTL RVVFEAYPMPSVLWLKDNRTLGD 358

QY 359 N-LTEITTDVEKIQEIRYSKLLIPAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSI 417
Db 359 SGAGELVLSTRNMSETRYVSELILVRVKVSEAGYITMRAFHEDEVQLSFKLQVNVVPRV 418

QY 418 LDLVDHGGSTGGQTVRCTAEGTPLPDIEWMICKDKKCNNETSWTILANNVSNIIITEIH 477
Db 419 LEL-SESHPANGEQTIRCRGRMPQPNVTWSTCRDLKRCPRKLSPTPLGNS----- 468

QY 478 SRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVAPTILR 522
Db 469 SKEESQLENTVTFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLP 528

QY 523 SELTVA AVLVLVIVIIISLIVLVVIWKQKPRYEIRWRVIESIPDGHEYIYVDPMLPY 582
Db 529 FKVVVISAILALVLTVISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPQLPY 588

QY 583 DSRWEFFRDGLVLRVLGSGAFGKVVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALM 642

Db 589 DSTWELPRDQLVLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALM 648
QY 643 SELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNLYLHKNRDSFLSHHPEK-- 700
Db 649 SELKIMSHLGPHLNVVNVLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKH 708

QY 701 -PKKELDIFGLNPADESTRSYVLLSFENNGDYMDMKQADTTQYVPMLEKVEVSKYSIDIOR 759
Db 709 PPSABLYSNAL-PVGFSLPShLNLTGESDGGYMDMSKDESIDYVPM LDKMDIKYADIES 767

QY 760 SLYDRPASYYKKSM L DSEVKM L L SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
Db 768 PSYMAPYDNYVPSAPERTYRATLIND-SPVLSYTDLVGFSYQVANGMDFLASKNCVHRDL 826

QY 820 AARNVLLAOGKIVKICDFGLARDIMHDSNVVSKGSTFLPVKWMAPESIFDNLTYTTLSDVW 879
Db 827 AARNVLICEGKLVKICDFGLARDIMRDSNYISKSTYLP LKWMAPESIFNSLYTTLSDVW 886

QY 880 SYGILLWEI FSLGGTPYPGMMVDSTFYNNIKKSGYRMAKPDHATSEVYEIMVKWNSEPEK 939
Db 887 SFGILLWEI FTLGGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKEFET 946

QY 940 RPSFYHLSEIVENLLPGQYKXSEYEKIHLDFLKSDDHPAVARMR-----VDSNA 987
Db 947 RPPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPALRSQARFPFGIHSRLRSP LDTSSV 1006

QY 988 YIGVTKNEEDKLKDWEGDLDEQRLSADSGYIIPLPDIDPVPEEEDL--GKRNRRHSSQTS 1045
Db 1007 LYTAVQPNE-----SDNDYIIPLPDPKPDVADEGLPEGSPSLASSTLN 1049

QY 1046 EESAIE TGSSSTFIKRED---ETIEDIDMDDDIGIDSS-DLVEDSFL 1089
Db 1050 EVNTSSTISCDSPLELOEERQAEPEAQLEQPDQSGCGPGLAEAE DSFL 1098

RESULT 7
T30815
platelet-derived growth factor receptor beta - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: T30815
R;How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A;Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for plat
A;Reference number: Z20882; MUID:97129405; PMID:8973913
A;Accession: T30815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1048 <HOW>
A;Cross-references: UNIPROT:P79749; EMBL:U63926; NID:G1752706; PID:G1752707; PIDN:AAC600
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

Query Match 38.6%; Score 2182.5; DB 2; Length 1048;
Best Local Similarity 43.9%; Pred. No. 1.5e-87;
Matches 472; Conservative 175; Mismatches 334; Indels 93; Gaps 25;

QY 9 LVLGCLLTGLSLILCQLSLPSILPNENEKVQVQLNSSFSRLRCFGESEVSWQ-----YPM 61
Db 16 VALAALLSSCTTVSCL----KIVPEEKQLILAESSLSLTGAGSSETTDLKSDDDVPFFQ 71

QY 62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYTCYNNHTQTEENELEGRHIYIYV 121
Db 72 MKAESSDLNYKIVQSNS--TASVLTLMHVWDKNTAVYQC-----REQLTGEIKEVAVFV 123

QY 122 PDPDVAFVPLGM----TDVLVIVEDDDSAIIPCRTTDPETPTVLHNSEGVVPAS--YDSR 175
Db 124 PD----RFSPQTLRFIESHGMVTKTSGESTVPCVVVTNPNITVTLYDKOTDLPVNGVVPS 180

QY 176 QGFNGTFTVGPYICEATVKGKFKQTIPTFNVYALKATSELDLEMEALKTVYKSGETIVVTC 235
Db 181 EGFKAYLDYRTYVCRGELNGEVKESQAFNVYSIHVPEDIDAYVNASQTVLKQGEPLTVNC 240

Db 130 NDTLVRCLPTDPEVTNYSLTGCEG-KPLPKDL-----TFVADPKAGITIRNVKREYHRL 182

QY 189 ---CEATVKGKKFQTIPFNV---YALKATSELDDLEMEALKTVY--KSGETIVVTCAVFN- 239

Db 183 CLHCSANQRKSMLSKKFTLKVRAAIKAVPVVSVS-----KTSYLLREGEFEFAVTCCLIKDV 238

QY 240 NEVVDLQWTPGGEVKGKGITMLLEEIKVPSIKLV--YTLTVPEATVVKDSDGYECAARQATR 297

Db 239 SSSVDSMMWIKENSQQTKAQTKKNSWHQDFFSYLRQERLTISSARVNDSGVFMCYANNTFG 298

QY 298 EVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPP-RISWLKNNLTIL 356

Db 299 SAN--VTITLEVVDKGFINIFPMNNTTVFVNDGENVDLVVEYEAYPKPVHRQWIYMNRTS 356

QY 357 IENLTTEITDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSS 416

Db 357 TDKWDDYPKS-ENESNIRYVNELHLTRLKGTEGGTYTFHVSNSDVNSSVTFNVVYVNTKPE 415

QY 417 ILDLVDHHGSGGTVRCTAEGTPLPDIEWMICDII-KKCNNETSWTILANNVSNIIITE 475

Db 416 ILT-----HDLRVNGMLQCVAAGFPEPTIDWYFCPGTEQRCVSP-----VGPVDVQ 461

QY 476 IHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE-----NRELKLVAPT 520

Db 462 IQNSSVSFPGKLVVYSTIDDSSTFKXNGTVECRAYNDVGKSSASFNAFKGNSKEQIHAHT 521

QY 521 LRSELTVAANAALLVLLVIVIIISLVLVVIWKQPRYEIRWRVIESISPDGHEYIYVDPMQ 580

Db 522 LFTPLLLIGFVIAAGLMCIVF--MILTYKYLQKPMYEQWKVVEEI--NGNNYVYIDPTQL 577

QY 581 PYDSRWEPRDGLVGRVLGSGAFGVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQA 640

Db 578 PYDHKWEPRNRLSFGKTLGAGAFGVVEATAYGLIKSDAAMTAVVKMLKPSAHLTEREA 637

QY 641 LMSELKIMTHLGPLHNIVNLLGACTKSGPIYIITEYCFYGDILVNLHKNRDSFLSHHPEK 700

Db 638 LMSELKVLVSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQED 697

QY 701 PKKELDIFGLNPADESTRSYVILSFENNGDYMMDKQADTTQYVPMLERKEVSKYSIDIORS 760

Db 698 HAEVALYKNLLHSKESSCN-----DSTNEYMDMKPG--VSIV-----VPTKADKRRS 742

QY 761 LYDRPASYYKKSMLDSEVKNLLSDDNSEGTLTLLDLLSFTYQVARGMEFLASKNCVHRDLA 820

Db 743 A--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLA 795

QY 821 ARNVLLAQGKIVKICDFGLARDIMHDSNVYSKGSTFLPVKNWAPESIFDNLYTTLSDVMS 880

Db 796 ARNILLTHGRITKICDFGLARDIKNDSNVYVKGARLPPVKWAPESIFNCVYTFESDVMS 855

QY 881 YGILLWEIFSLGGTPYPGMVVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKR 940

Db 856 YGIFLWELFSLGSSPYPGMPVDSKFYKVIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKR 915

QY 941 PSFYHLSEIVENLLPGQYKKSXEKIHLDLFLKSDHPAVAR-MRVDS 984

Db 916 PTFKQIVQLIEKQISESTNHIYSLANCSPHRENPAVDHSVRINS 960

RESULT 10

JN0677

protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken

N;Alternate names: tyrosine kinase receptor kit

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JN0677

R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Sakurai, M

Gene 128, 257-261, 1993

A;Title: Cloning and expression of the chicken c-kit proto-oncogene.

A;Reference number: JN0677; MUID:93292995; PMID:7685729

A;Accession: JN0677

A;Molecule type: mRNA

A;Residues: 1-960 <SAS>

A;Cross-references: UNIPROT:Q08156; DDBJ:D13225; NID:g303532; PIDN:BAA02506.1; PID:g303535

A;Experimental source: brain

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; rotein kinase

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>

F;314-380/Domain: immunoglobulin homology <IMM>

F;573-916/Domain: protein kinase homology <KIN>

F;581-589/Region: protein kinase ATP-binding motif

F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)

Query Match 25.9%; Score 1461.5; DB 1; Length 960;

Best Local Similarity 36.1%; Pred. No. 2.9e-56;

Matches 365; Conservative 148; Mismatches 359; Indels 139; Gaps 30;

QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVLNSSFSLRCFGESEVSWQYP 60

Db 1 MEGAHLAWELAHAVLL-LSLIPAGGSVPH--EESSLVYNKGEELRLKCNEEGPVTWNF- 55

QY 61 MSBEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENELEG---RHI 117

Db 56 QNSDPSAKTRISNEKE-----WHTKNATIRDIGYEC-----KSKGSIVNSF 97

QY 118 YIYVDPDPDAFVPLGMDTVLIVIVEDDDSAIIPCRTTDPET-PVTLHNSEG-VVPASVDSR 175

Db 98 YVFPKDPNVLF---LVDSLITYGKEDSDILLVCPLTDPDLNFTLRKCDGKPLPK----- 148

QY 176 QGFNGTFTVGP-----YICEATVKG--KKFQTIPFNVYAL-KATSELDL 216

Db 149 ---NMTFIPNPQGIIIKNVQRSFKGCYQCLAKHNGVEKISEHIFLNVRPVHKALPVITL 205

QY 217 EMEALKTVYKSGETIVVTCAVFNNEVVDLQWTPGGEVKGKGITMLEEIKVPSIKLV--- 272

Db 206 SKS--YELLKEGEEFEVTCIITD---VD-----SSVKASWISYKSAIVTSKSRNLGDYG 254

QY 273 ----YTLTVPEATVKDSDGYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVN 328

Db 255 YERKLTILNIRSVGVNDSGEFTCQAEHPFG--KTNATVTLKALAKGFVRLFATWNTTIDIN 312

QY 329 LHEVKHFVVEVRAYPPPRIS-WLKNNLTLIENLTTEITDVEKIQEIRYRSKLLIRAKEE 387

Db 313 AQQNGNLTVYEYAYPKPKEEVMWYMNETL-QNSSDHVYVKFTVGNNSYTSSELHLTRLKGT 371

QY 388 DSGHYTIVAQNEDAVKSYTFELLTQVPSSILDVDDHHGSGGTVRCTAEGTPLPDIEW 447

Db 372 EGGIYTFVVSNSDASSSVTFNVVYVTKKPEILTL----DMLGNDILQCVATGFPAPTYY 426

QY 448 MICKDI-KKCNNETSWTILANNVSNIIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNL 506

Db 427 YFCPGTEQRCLDSPITSPMDVKVSYTNSVPSFERILLVESTVNASMFKSTGTICCEA--- 483

QY 507 LGAENRELKV-----APTLRSELTVAANAALLVLLVIVIIISLVLVVIWKQPRY 555

Db 484 --SSNGDKSSVFFENFAIKEQIRTHTLFTPLLIAFGVAAGLMCIIV--MILVYIYLQPKY 539

QY 556 EIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVGRVLGSGAFGVVEGTAYGL 615

Db 540 EVQWKVVEEI--NGNNYVVIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGVVEATAYGL 597

QY 616 SRSQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNIVNLLGACTKSGPIYIITE 675

Db 598 FKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSYLGNHINIVNLLGACTIGGPTLVITE 657

QY 676 YCFYGDILVNLHKNRDSFL---SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDY 731

Db 658 YCCYGDLLNFLRRKRDSFICPKHEEHAAEAAYENLLHQAEPTADAV-----NEY 706

QY 732 MDMKQADTTQYVPMLERKEVSKYSIDIORSLYDRPASYYKKSMLDSEVKNLLSDDNSEG 791

Db 707 MDMKPGVSYAVPPKADKK-----RPV--KSGSYTDQDVTLSMLEDDDELALD 750

A;Cross-references: GB:S78839; NID:g244084; PIDN:AAB21234.1; PID:g244085
A;Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBIP:78842)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: B41815
A;Molecule type: DNA
A;Residues: 637-641,'SPELPW' <SP2>
A;Cross-references: GB:S78843; NID:g244086; PIDN:AAB21235.1; PID:g244087
A;Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBIP:78844)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: C41815
A;Molecule type: DNA
A;Residues: 556-560,'GCDKWK' <SP3>
A;Cross-references: GB:S78845; NID:g244088; PIDN:AAB21236.1; PID:g244089
A;Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBIP:78846)
A;Note: disease-related mutant from patient with piebaldism
R;Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.
Oncogene 7, 2207-2217, 1992
A;Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth fa
A;Reference number: I37948; MUID:93064697; PMID:1279499
A;Accession: I37948
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-976 <RES>
A;Cross-references: EMBL:X69301; NID:g34089; PIDN:CAA49159.1; PID:g825686
A;Note: an alternative splice form omitting residues 510-513 is described
R;Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M.
Jpn. J. Cancer Res. 84, 1136-1144, 1993
A;Title: Characterization of the promoter region of the human c-kit proto-oncogene.
A;Reference number: I56954; MUID:94103107; PMID:7506248
A;Accession: I56954
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RE2>
A;Cross-references: GB:S67773; NID:g459358; PIDN:AAB29529.1; PID:g459359
R;Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.
Hum. Mol. Genet. 2, 1499-1500, 1993
A;Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-c
A;Reference number: I54336; MUID:94061059; PMID:7694728
A;Accession: I54336
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 242-250 <RE3>
A;Cross-references: GB:S67686; NID:g460545; PIDN:AAD13996.1; PID:g4261696
C;Genetics:
A;Gene: GDB:KIT
A;Cross-references: GDB:120117; OMIM:164920
A;Map position: 4q12-4q12
A;Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1; 6
A;Note: defects in this gene may result in piebaldism
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related
rotein; tyrosine-specific protein kinase
F;1-976/Product: protein-tyrosine kinase kit precursor, long form #status predicted <MAT
F;1-509,514-976/Product: protein-tyrosine kinase kit precursor, short form #status predi
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-976/Product: protein-tyrosine kinase kit #status predicted <MAT>
F;23-520/Domain: extracellular #status predicted <EXT>
F;51-99/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;226-292/Domain: immunoglobulin homology <IMM3>
F;328-394/Domain: immunoglobulin homology <IMM4>
F;423-493/Domain: immunoglobulin homology <IMM5>
F;521-543/Domain: transmembrane #status predicted <TM>
F;544-976/Domain: intracellular #status predicted <INT>
F;587-931/Domain: protein kinase homology <KIN>
F;595-603/Region: protein kinase ATP-binding motif
F;58-97,136-186,233-290,428-491/Disulfide bonds: #status predicted
F;130,145,283,293,300,320,352,367,463,486/Binding site: carbohydrate (Asn) (covalent) #s
F;623,640,792/Active site: Lys, Glu, Asp #status predicted
F;797,810/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.7%; Score 1454.5; DB 1; Length 976;
Best Local Similarity 35.7%; Pred. No. 5.9e-56;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;

Qy 26 SLPSILPNENKVVQLNSPSILRCFGESEVSWQYPMSEESSDVEIRNEENNSGLFVTVL 85
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 35 SPSPHHPGKSDLIVRGDEIRLLCTDPGFVKWTFEILDE-----TNENKQNEWIT-- 84
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 86 EVSSASAAHTGLYTCYNNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLIVEDDSD 145
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 85 --EKAETNTGKYTCNTKHGLSNS-----IYFVRDPAKLF---LVDRSLYGKEDND 131
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 146 AIIPCRTTDPE-TPVTLHNSGVVVPASYDSRQGFNGTFTVGPYI----- 188
: : | | | | | : : | | | | | : : | | | | | : : | | | | |
Db 132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR-----FIDPKAGIMIKSVKRAYHRLCL 184
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 185 HCSVDQEGKSVLSEKFIKVRPAFAKAVPVVSVSKASY--LLREGGEFTVTCTIKDVSSSV 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 240 -----NEVDLQWTPGVEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYEC 292
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 243 YSTWKRENSQTKLQEKYNSWHHGDG-----NYERQATLTISSARVNDSGVFMCYA 292
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 293 RQATREVKEMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVWEVRAYP-PPRISWLK 351
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFFKPEHQWIY 350
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 352 NNLTLIENLTEITDVEKIQEIRYRSKLIRAKEEDSGHVTIVAQNEDAVKSYTFELLT 411
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTGCTYTFVLSNSDVNAIAFNVV 409
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 412 QVPSSILD--LVDDHHGSGGTVRCTAEGTPLPLDIEWMICKDIKKCNNETSWTILANN 468
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 410 NTKPEILTYDRLVNG-----MLQCVAAAGFPEPTIDWYFCPGTEQ---RCSASVL 458
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 469 VSNITIEHSRRDRSTVEGRVTFKAEETIAVRCLAKNLLGAE-----NRELK 518
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNAFKGNKEQIHP 518
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 519 PTLRSELTVAAAVLVLLVIVLIVLVIWKQPRYBIRWRVIESISPDGHEIYIVDPM 578
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 519 HTLFTPLLLIGFVIVAGMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVIDPT 574
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 579 QLPYDSRWEFPRDGLVLRVLGSGAFGKVGVEGTAYGLSRSQPVMKAVKMLKPTARSSEK 638
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 639 QALMSELKIMTHLGPLHNLVNLGACTKSGPIYIITBXYCYGDLVNLHKNRDSFLSHHP 698
: : | | | | | : : | | | | | : : | | | | | : : | | | | |
Db 635 EALMSELKVL SylGNHNMVNLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDKQADTTQYVPMLEKEVSKYSDIQ 758
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 695 EDHAEALYKNLLHKSSECS-----DSTNEYMDMKPG--VSIV-----VPTKADKR 739
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 759 RSLYDRPASYYKKKSMLDSEVKNLLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRD 818
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 740 RSV--RIGSY-----IERDVTTPAIMEDELALDLEDLLSFSYQVAKGMFLASKNCIHRD 792
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 819 LAARNVLLAQKIVKICDFGLARDIMHDSNYVSKSTFLPVKWMAPESIFDNLTYTLSDV 878
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 879 WSYGILLWEIFSLGGTYPGMVVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPE 938
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 853 WSYGIFLWELFSLGSSYPGMPVDKFKYKMIKEGFRMLSPAHAPAEYDIMKTCWDADPL 912
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 913 KRPTFKQIVQLIEKQISESTNHIYSNL 939
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 13
TWMSKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N;Alternate names: tyrosine kinase receptor c-kit
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S00474; B44876; I49596
R;Qiu, F.; Ray, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Besmer, P.
EMBO J. 7, 1003-1011, 1988
A;Title: Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase fa
A;Reference number: S00474; MUID:88296403; PMID:2456920
A;Accession: S00474
A;Molecule type: mRNA
A;Residues: 1-975 <QIU>
A;Cross-references: UNIPROT:P05532; GB:Y00864; NID:G50423; PIDN:CAA68772.1; PID:G50424
R;Rossi, P.; Marziani, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A;Title: A novel c-kit transcript, potentially encoding a truncated receptor, originates
A;Reference number: A44876; MUID:92331813; PMID:1378413
A;Accession: B44876
A;Molecule type: DNA
A;Residues: 771-814 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIN:108837, NCBI:P:108840)
R;Yasuda, H.; Galli, S.J.; Geissler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A;Title: Cloning and functional analysis of the mouse c-kit promoter.
A;Reference number: I49596; MUID:93221533; PMID:7682073
A;Accession: I49596
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:L11358; NID:G2933325; PIDN:AAA37420.1; PID:G2933326
C;Genetics:
A;Gene: kit; c-kit
A;Map position: 5
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-975/Product: protein-tyrosine kinase kit #status predicted <KTC>
F;23-519/Domain: extracellular #status predicted <EXT>
F;51-100/Domain: immunoglobulin homology <IMM1>
F;130-189/Domain: immunoglobulin homology <IMM2>
F;227-295/Domain: immunoglobulin homology <IMM3>
F;331-397/Domain: immunoglobulin homology <IMM4>
F;426-496/Domain: immunoglobulin homology <IMM5>
F;520-542/Domain: transmembrane #status predicted <TMW>
F;543-975/Domain: intracellular #status predicted <INT>
F;586-929/Domain: protein kinase homology <KIN>
F;594-602/Region: protein kinase ATP-binding motif
F;58-98,137-187,234-293,431-494/Disulfide bonds: #status predicted
F;146,296,303,323,355,370,466,489/Binding site: carbohydrate (Asn) (covalent) #status pr
F;622,639,790/Active site: Lys, Glu, Asp #status predicted
F;795,808/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.6%; Score 1446.5; DB 1; Length 975;
Best Local Similarity 35.7%; Pred. No. 1.3e-55;
Matches 357; Conservative 152; Mismatches 374; Indels 117; Gaps 29;

QY 26 SLPSILPNENEKVQLNSSFSLRFCGESEVSWQYPMSEBSSDVEIRNEENNSGLFTTVL 85
| | | | : : : : | | | | : : : : | | : : : :
Db 35 SPFSIHPAQSELIVEAGDTLSLTCLDPDFVRWTFTKTYFNEM-----VENKKNE-----WIQ 85
| | | | : : : : | | | | : : : : | | : : : :
QY 86 EVSSASAHTGLYTCYNHHTQTEENELEGRHIYYVPDPDVAFVPLGMDTYLVIVEDDDSD 145
| | | | : : : : | | | | : : : : | | : : : :
Db 86 E--KAEATRTGTYTCSNSNGLTSS-----IYFVRDPAKLFL-VGLP---LFGKEDSD 132
| | | | : : : : | | | | : : : : | | : : : :
QY 146 AIIPCRTTDPE-TPVTLHNSEG-VVPASYDSRQGFNGTFTVGPYI----- 188
| : : | : : : : | : : : : | | : : : :
Db 133 ALVRCPLTDPQVSNYSLEICDGKSLPTDL-----TFVPNPKAGITIKNVKRAYHRLC 184
| | | | : : : : | | : : : : | | : : : :
QY 189 --CEATVKGKKFQTIPFNVVYALKATSELD-LEMEALKTVYKSGETIVWTCAVFN-NEVVD 244
| | | | : : : : | | : : : : | | : : : :

Db 185 VRCAAQRDGTWLHSDKFTLLKVBREAIIKAI PVVSV PETSHLLKKGDTFTVVCTIKDVSTSVN 244
QY 245 LQW-----TYPGEVK---GKGITMLEEIKVPSIKLVTLTVPEATVKDSGDYECAAR 293
| | | | : : : : | | | | : : : : | | : : : :
Db 245 SMWLKMNPPQHIAQVKHNSWHRGDFNYERQE-----TLTISSARVDDSGVFMCYAN 296
QY 294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKN 352
| | | | : : : : | | | | : : : : | | : : : :
Db 297 NTFGSAN--VTTTLKVVEKGFINISPVKNTTVTFVTDGENVDLVVEYEAYPKPEHQQWIYM 354
QY 353 NLTLIENLTEITTOVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412
| | | | : : : : | | | | : : : : | | : : : :
Db 355 NRTSANKGKDYVKSDNK-SNIRYVNLRLRLTKGTGGTYTFLVSNSDASASVTFNVYVN 413
QY 413 VPSSILDLDVDDHHGSTGGTVRCTAEGTLPDIEWMICKDI-KKCNNETS-WTILANNVS 470
| | | | : : : : | | | | : : : : | | : : : :
Db 414 TKPEILTYDRLING-----MLQCVAGGFPEPTIDWYFCTGAEQRCTTPVSPVDVQVQNV 468
QY 471 NIITEIHSRDRSTVEGRVTFKAVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
| | | | : : : : | | | | : : : : | | : : : :
Db 469 -----VSPFGKLVVQSSIDSSVFRHNGTVECKASNDVGKSSAPFNAFKEIQIAHTLFTP 523
QY 531 VLVLLVIV--IISLIVLVVWK--QKPRYEIRWRVIESIPDGHEIYYVDPMQLPYDSRW 586
| | | | : : : : | | | | : : : : | | : : : :
Db 524 LLIGFWAAGAMGIIVMVLTYKYLQKPMYEVQWKVVEEI--NGNYYVYIDPTQLPYDHW 581
QY 587 EFPRDGLVLRVLGSGAFGKVEGTAYGLSRSQPVMMKVAVMKLPKTARSSEKQALMSELK 646
| | | | : : : : | | | | : : : : | | : : : :
Db 582 EPPNRLSFGKTLGAGAFGKVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELK 641
QY 647 IMTHLGPHLNIIVNLGACTKSGPIYIITEYCFYGDLVNVLHKNRDSFLSHHPEKPKKELD 706
| | | | : : : : | | | | : : : : | | : : : :
Db 642 VLSYLGNMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSEFISKQEEQAEAL 701
QY 707 IFGLNPADESTRSYVILSPENNGDYMDMKQADTTQYVPMLEKESKYSDIQRSLYDRPA 766
| | | | : : : : | | | | : : : : | | : : : :
Db 702 YKNLLHSTEP-----SCDSSNEYMDMKPG-VSYVVP-----TKTDKRR 738
QY 767 SYKKKSMLDSEVKNLLSDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLL 826
| | | | : : : : | | | | : : : : | | : : : :
Db 739 SARIDSYIERDVTPAIMEDDELALDLDLLSFSYQYAKAMAFLASKNCIHRDLAARNILL 798
QY 827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLW 886
| | | | : : : : | | | | : : : : | | : : : :
Db 799 THGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFSCVYTFESDVWSYGIFLW 858
QY 887 EIFSLGGTYPYPGMMVDSYFNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSPFVHL 946
| | | | : : : : | | | | : : : : | | : : : :
Db 859 ELFSLGSSPYPGMPVDSKFYKMIKEGFRMVSPEHAPAEYMDVMKTCWDADPLKRPTFKQV 918
QY 947 SEIVENLLPGQYKKSYEKIHLDFLKS DHPAVA--RMRVDS 984
| | | | : : : : | | | | : : : : | | : : : :
Db 919 VQLIEKQISDSTKHIYSNLANCNPENPNPVVVDHHSVRVNS 958
RESULT 14
I51703
c-kit-related kinase 1 (XKrk1) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51703
R;Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
Mech. Dev. 50, 217-228, 1995
A;Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem cel
A;Reference number: I51703; MUID:95344996; PMID:7619732
A;Accession: I51703
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-954 <BAK>
A;Cross-references: UNIPROT:Q91909; EMBL:Z48770; NID:G763033; PIDN:CAA89688.1; PID:G76303;
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP
F;575-915/Domain: protein kinase homology <KIN>

F:583-591/Region: protein kinase ATP-binding motif

Query Match 25.1%; Score 1416.5; DB 2; Length 954;
 Best Local Similarity 36.4%; Pred. No. 2.6e-54;
 Matches 361; Conservative 157; Mismatches 368; Indels 107; Gaps 32;

QY	26	SLPSILPNEKVVQLNSSFS	LCFGESEVSWQY	PMS--EEESSDVEIR--NEENNSGLF	81
DB	19	AVPKINDGEDRVTVNVGD	KVSLKCRDAHLVT	LAFOKSLMKKPRDLKSRPLNNSETDQFF	78
QY	82	VTVLEVSSASAAHTGLY	TCYNNHTQTEENELEGR	HIYIVYDPDPAFVPLGMTDYLIVE	141
DB	79	VII-----KADLRHGRY	IC--TNTETQEN-----	TSVSLFVKDPAFPFLDIPFID----	VT 124
QY	142	DDDSAILPCRTTDPETP	VTLHNSEG--VVPASYDS	RQGFNGTFTV-----GPYICEAT	192
DB	125	EGADTVGCMCFPTDPM	DMDIAIEKCDGSPLEN	FTTFTDIEAGITIKTVQLAFDSCYVCSGN	184
QY	193	VKGKKFQTIPIPNVYAL	KATSEL--DLEMEALKTV	YKSGETIVVTCAVFN--NEVVDLQWYTP	250
DB	185	KSGTVKKSSTFSIHVK	VPVKVPTVFLSKSRQL	VKTGEPFEVTCVLDVFSVKAQWL--	242
QY	251	GEVKGKGITMLEEIKV	PSIKLVYTLTVPEATV--	KDSGDYECARQATREVEMKKVITIS	308
DB	243	-DVK-EGVTKQANFR	SSNV--FSYNLTLSK	DGVPSRSRTFTCQAEANAIGQVN--ATFTLD	297
QY	309	VHEKGFIKPTFSQLEA	VNLHEVKHFVVEVRA	YPPPRIS--WLKNNLTLIENLTETTDV	367
DB	298	VIDVGYNLTVLENTIS	VNAGDNLVLKVYID	AYPHPDGVTYFNETLL--NTSDHYVAT	356
QY	368	EKIQEIYRSKLIRAKE	EDSGHYTIVAQNEDAV	KSYTFELLTQVPSSILDLVDHHS	427
DB	357	KDEGNRYVSELHLRL	KGTEKGVYTFYTTNS	DDASVSFNIQVTRPEILIAERTSEG--	415
QY	428	TGGQTVRCTAEGTPL	PDIEWMICK--DIKKCN	NETSWTILANNVSNIIITEIHSRDRSTVEG	486
DB	416	---TLQCVATGTFV	PAIQWYFCPGSEQR	C---TDYPLSPVNEKFIQENSSLGRIVVES	468
QY	487	RVTFAKVEETIAVR	CLAKNLLGAENR-----	ELKLVAPTLRSELT---VAAAVLVLLVI	537
DB	469	TIDVNDLKNGTVQC	VASNEVESAYSVFS	PAIKEKURTHLTFTPLLLIGFIAAAGL----	523
QY	538	VIIISLIVLVVWKQ	PRYIEIRWRVIESI	SPDGHEYIVYDPMQLPYDSRWEFPRDGLVGR	597
DB	524	MCIATAVLMYKYLQ	KPKYIEIQWKVVEE	I--NGNNVYVIDPTQLPYDNKWEFPRDRLCFGK	581
QY	598	VLGSGAFGKVVVEG	FAYGLSRSQPVMKV	AVKMLKPTARSSEKQALMSELKIMTHLGPLNI	657
DB	582	ILGAGAFGKVVEAT	AYGLLKEDSRLT	VAVKMLKPSAHSTEREALMSELKVL SylGHHKNI	641
QY	658	VNLLGACTKSGPIY	ITEYCFYGDVNYLH	KNRDSFLSHHPEKPK---KELDIFG--LN	711
DB	642	VNLLGACTVGGPTL	VITEYCCYGDLLN	YLRRKRDSFIC----PKFEDNSEAALYKNLLN	696
QY	712	PADESTRSVVILS	PENNGDYMMDKQAD	TTQYVPMLEKVEVSKYSIDIQRSLYDRPASVKKK	771
DB	697	TRD-----MGCEG	MEYIDMKPA--VS	YV-----VPTKTDKRRS-----G	729
QY	772	SMLDSEVKNLLSDD	NSEGLTLLDLLS	FTYQVARGMEFFLASKNCVHRDLAARNVLLAQGI	831
DB	730	SFGDQDVSVSIP	EDDLALDTEDLIN	FSYQVAGNMFLASKNCIHRDLAARNILLTHGRI	789
QY	832	VKICDFGLARDIM	HSNYSVSGSTFLP	VKWMAPESIFDNLYTTLSDVWSYGILLWEIFSL	891
DB	790	TKICDFGLARDIR	NDNSYVVKGNARL	PVKWMAPESIFHCVYTFESDVWSYGILLWEIFSL	849
QY	892	GGTPYPGMMVDST	FYNKIKSGYRMAK	PDHATSEVYEIMVKWCNSEPEKRPSFYHLSEIVE	951
DB	850	GSSPYPRIPVDS	KFYKMIKDGVRM	MSPECAPLEMYEIMRSCWNSDPLKRPTFKQIVQMV	909
QY	952	NLLPGQYKKS	YEKIHLDFLKSD	HPAVARMRVD	984
DB	910	Q-----QLSDSK	GNWTPLPYPVSH	VPLDHA VRINS	938

RESULT 15
TVCTMD
macrophage colony-stimulating factor 1 receptor precursor - cat
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms
C:Species: Felis silvestris catus (domestic cat)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31636
R:Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A:Title: Activation of the feline c-fms proto-oncogene: multiple alterations are required
A:Reference number: A31636; MUID:89077553; PMID:2849512
A:Accession: A31636
A:Molecule type: mRNA
A:Residues: 1-980 <WOO>
A:Cross-references: UNIPROT:P13369; EMBL:X03663
C:Genetics:
A:Gene: fms
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT>
F:24-509/Domain: extracellular #status predicted <EXT>
F:35-86/Domain: immunoglobulin homology <IMM1>
F:120-179/Domain: immunoglobulin homology <IMM2>
F:217-280/Domain: immunoglobulin homology <IMM3>
F:316-381/Domain: immunoglobulin homology <IMM4>
F:410-484/Domain: immunoglobulin homology <IMM5>
F:510-534/Domain: transmembrane #status predicted <TMM>
F:535-980/Domain: intracellular #status predicted <INT>
F:577-915/Domain: protein kinase homology <KIN>
F:585-593/Region: protein kinase ATP-binding motif
F:42-84, 127-177, 224-278, 417-482/Disulfide bonds: #status predicted
F:45, 73, 94, 153, 275, 302, 335, 410, 477, 490/Binding site: carbohydrate (Asn) (covalent) #status
F:613, 630, 776/Active site: Lys, Glu, Asp #status predicted
F:781, 794/Binding site: magnesium (Asn, Asp) #status predicted

Db

Db 407 TLIN-----GSDTLCEASGYQPQSVTWVQCRSHTDRCDSEAGLVLEDSSHSEVLSQVPF 460

Qy 479 RDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENR---ELKLVAPT-LRSELTVAANAIVLV 534

Db 461 HE-VIVHSLLAIGTLEHNRITYECRAFNSVGNSSQTFWPISIGAHTQLPDELLFTPVLLTC 519

Qy 535 LVIVIISLIVLVI---WKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEPFRD 591

Db 520 MSIMALLLLLLLLLYKYKQKPKYQVRWKIIESY--EGNSYTFIDPTQLPYNEKWEFPRN 577

Qy 592 GLVLGRVLGSAFGKVGWEGTAYGLSRSPVMKVAVKMLKPTARSSKQALMSELKIMTHL 651

Db 578 NLQFGKTLGAGAFGKVEATAFGLGKEDAVLKVAVKMLKSTAHADKEALMSELKIMSHL 637

Qy 652 GPHLNIVNLGACTKSGPIYIITEYCFYGDVNLVNLHKNRDSFLSHHPEKPKKELDIFGLN 711

Db 638 QOHENIVNLGACTHGGPVLVITEYCCYGDLLNFLRRQAEAMLG-----PSLSV-GQD 689

Qy 712 PADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSIDIQRSLYD-----RPA 766

Db 690 P-----EAGAGYKNIH-----LEKKYVRRDSFSSQGVDTYVEMRPV 726

Qy 767 SYKKKSMLDSEVKNLLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLL 826

Db 727 S--TSSSNDSPSEEDLGKEDGRPLELRDLHFSSQVAQGMFLASKNCIHRDVAARNVLL 784

Qy 827 AQKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLVTTLSDVWSYGILLW 886

Db 785 TSGRVAKIGDFGLARDIMNDSNYIVKGNARLPVKWMAPESIFDCVYTVQSDVWSYGILLW 844

Qy 887 EIFSLGGTPYPGMMVDSTFYNNIKISGYRMAKPDHATSEVYEIMVKCWNSEPEKRPFSYHL 946

Db 845 EIFSLGLNPYPGILVNSKFYKLVKDGYNQAPAFAPKNIYSIMQACWALEPTRRPTFQOI 904

Qy 947 SEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVSDNAYIGVYKNEEDKLKWEGG 1006

Db 905 CSLLQK-----QAQEDR----- 916

Qy 1007 LDEQRLSADSGYIIPDPIDVPPEEEDLGKRNHRSSQTSSESAIETGSSSSSTFIKREDET 1066

Db 917 -----RVPNYTNLPSS-----SSSSSSSSSCTGSGGSSSEPEEES 954

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:17:30 ; Search time 74.0692 Seconds
(without alignments)
4925.234 Million cell updates/sec

Title: US-10-027-400-4
Perfect score: 5766
Sequence: 1 MRLPGAMPALALKGELLLLS.....EQLPDSGCPAPRAEADSFL 1106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5766	100.0	1106	14 US-10-027-400-4	Sequence 4, Appli
2	5762	99.9	1106	9 US-09-955-363-2	Sequence 2, Appli
3	5762	99.9	1106	15 US-10-394-322A-51	Sequence 51, Appli
4	5762	99.9	1106	15 US-10-367-639-36	Sequence 36, Appli
5	5760	99.9	1106	9 US-09-866-510-22	Sequence 22, Appli
6	5758	99.9	1106	9 US-09-866-510-16	Sequence 16, Appli
7	5757	99.8	1106	9 US-09-866-510-20	Sequence 20, Appli
8	5756	99.8	1106	9 US-09-866-510-18	Sequence 18, Appli
9	5676	98.4	1090	9 US-09-866-510-14	Sequence 14, Appli
10	2882	50.0	561	9 US-09-866-510-24	Sequence 24, Appli
11	2352.5	40.8	1089	9 US-09-866-510-10	Sequence 10, Appli
12	2351.5	40.8	1089	9 US-09-769-987-2	Sequence 2, Appli
13	2351.5	40.8	1089	9 US-09-919-497-90	Sequence 90, Appli

14	2351.5	40.8	1089	9 US-09-866-510-2	Sequence 2, Appli
15	2351.5	40.8	1089	9 US-09-955-363-36	Sequence 36, Appli
16	2351.5	40.8	1089	14 US-10-027-400-2	Sequence 2, Appli
17	2351.5	40.8	1089	15 US-10-394-322A-50	Sequence 50, Appli
18	2351.5	40.8	1089	15 US-10-367-639-35	Sequence 35, Appli
19	2351.5	40.8	1089	16 US-10-322-696-168	Sequence 168, App
20	2351.5	40.8	1089	16 US-10-741-601-439	Sequence 439, App
21	2351.5	40.8	1089	17 US-10-741-600-1304	Sequence 1304, App
22	2350	40.8	1088	10 US-09-961-403-4	Sequence 4, Appli
23	2347.5	40.7	1089	9 US-09-866-510-4	Sequence 4, Appli
24	2346.5	40.7	1089	9 US-09-866-510-8	Sequence 8, Appli
25	2345.5	40.7	1089	9 US-09-866-510-6	Sequence 6, Appli
26	2292.5	39.8	1096	16 US-10-322-696-165	Sequence 165, App
27	1499.5	26.0	460	16 US-10-664-421-64	Sequence 64, Appli
28	1400.5	24.3	976	13 US-10-099-895-32	Sequence 32, Appli
29	1400.5	24.3	976	14 US-10-192-867-4	Sequence 4, Appli
30	1400.5	24.3	976	15 US-10-295-027-708	Sequence 708, App
31	1400.5	24.3	976	15 US-10-457-954-2	Sequence 2, Appli
32	1385.5	24.0	811	15 US-10-637-356-4	Sequence 4, Appli
33	1383.5	24.0	826	15 US-10-637-356-3	Sequence 3, Appli
34	1382.5	24.0	975	14 US-10-192-867-2	Sequence 2, Appli
35	1380	23.9	834	15 US-10-637-356-2	Sequence 2, Appli
36	1380	23.9	849	15 US-10-637-356-1	Sequence 1, Appli
37	1370.5	23.8	972	9 US-09-944-807-10	Sequence 10, Appli
38	1370.5	23.8	972	17 US-10-741-600-1570	Sequence 1570, Ap
39	1370.5	23.8	972	17 US-10-741-600-1571	Sequence 1571, Ap
40	1306	22.7	806	16 US-10-408-765A-2335	Sequence 2335, Ap
41	1287.5	22.3	386	9 US-09-939-754-6	Sequence 6, Appli
42	1287.5	22.3	386	9 US-09-939-832-6	Sequence 6, Appli
43	1287.5	22.3	386	9 US-09-939-833-6	Sequence 6, Appli
44	1138	19.7	1333	15 US-10-394-322A-65	Sequence 65, Appli
45	1133	19.6	1302	15 US-10-402-365-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-027-400-4
; Sequence 4, Application US/10027400
; Publication No. US20030017535A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,400
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400

Db 1 MRLPGAMPALALKGELLLSLLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPEQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLGLETDERKRLYIFV 120
Db 61 VWERMSQEPPEQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLGLETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAEELFIFLTFITPCRVTDQQLVVTLHEKKGDDVALVPYDQHQRGS 180
Db 121 PDPTVGFLPNDAEELFIFLTFITPCRVTDQQLVVTLHEKKGDDVALVPYDQHQRGS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDGTYTCNVTESVNDH 300
Db 241 EVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDGTYTCNVTESVNDH 300
QY 301 QDEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAQVQLSFQLQINVPVRV 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAQVQLSFQLQINVPVRV 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 1081 EPEPELEQLPDSCGPAPRAEAEDSFL 1106
|||||

Db 1081 EPEPELEQLPDSCGPAPRAEAEDSFL 1106
RESULT 3
US-10-394-322A-51
; Sequence 51, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-51
Query Match 99.9%; Score 5762; DB 15; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALALKGELLLSLLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKGELLLSLLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPEQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLGLETDERKRLYIFV 120
Db 61 VWERMSQEPPEQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLGLETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAEELFIFLTFITPCRVTDQQLVVTLHEKKGDDVALVPYDQHQRGS 180
Db 121 PDPTVGFLPNDAEELFIFLTFITPCRVTDQQLVVTLHEKKGDDVALVPYDQHQRGS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDGTYTCNVTESVNDH 300
Db 241 EVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDGTYTCNVTESVNDH 300
QY 301 QDEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAQVQLSFQLQINVPVRV 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAQVQLSFQLQINVPVRV 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVTNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDDRPPPSAELYSNAL 720
|||||

Db	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL	720
Qy	721	PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP	780
Db	721	PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP	780
Qy	781	SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Db	781	SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Qy	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Db	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Qy	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER	960
Db	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER	960
Qy	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPPLDTSSVLYTAVQPNEGDND	1020
Db	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPPLDTSSVLYTAVQPNEGDND	1020
Qy	1021	YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080
Db	1021	YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080
Qy	1081	EPEPELQPLDSCGPAPRAEAEDSFL	1106
Db	1081	EPEPELQPLDSCGPAPRAEAEDSFL	1106
RESULT 4			
US-10-367-639-36			
; Sequence 36, Application US/10367639			
; Publication No. US2004001807A1			
; GENERAL INFORMATION:			
; APPLICANT: Cornell Research Foundation, Inc.			
; APPLICANT: Edelberg, Jay M.			
; APPLICANT: Rafii, Shahin			
; APPLICANT: Hong, Mun K.			
; APPLICANT: Lanza, Robert P.			
; APPLICANT: West, Michael D.			
; TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular			
; FILE REFERENCE: 1676.004US1			
; CURRENT APPLICATION NUMBER: US/10/367,639			
; CURRENT FILING DATE: 2003-02-13			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 36			
; LENGTH: 1106			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-367-639-36			
Query Match			
Best Local Similarity 99.9%; Score 5762; DB 15; Length 1106;			
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MRLPGAMPALAKGELL LLSLL LLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV	60
Db	1	MRLPGAMPALAKGELL LLSLL LLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV	60
Qy	61	VWERMSQEPQEMAKAQDGT FSSVLTLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120
Db	61	VWERMSQEPQEMAKAQDGT FSSVLTLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120
Qy	121	PDPTVGFLPNDAELFIFL TEITIPCRVTD PQLVVTLHEKGDVALPVYDHQRF	180
Db	121	PDPTVGFLPNDAELFIFL TEITIPCRVTD PQLVVTLHEKGDVALPVYDHQRF	180
Qy	181	GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240

Db	181	GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Qy	241	DVVNFWTYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTYTCNVTESVNDH	300
Db	241	EVVNFWTYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTYTCNVTESVNDH	300
Qy	301	QDEKAINITVVESGYVRLGEGTQLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD	360
Db	301	QDEKAINITVVESGYVRLGEGTQLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD	360
Qy	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRV	420
Db	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRV	420
Qy	421	ELSESHDPSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Db	421	ELSESHDPSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Qy	481	TYWEEQEFVSTLRLQHVDRPLSVRCCTLRNAVQDQTQEVIVVPHSLPFKVVVISAILA	540
Db	481	TYWEEQEFVSTLRLQHVDRPLSVRCCTLRNAVQDQTQEVIVVPHSLPFKVVVISAILA	540
Qy	541	LVVLTIIISLIILIMLWQKPRYIRWKVIESVSSDGHGYIYVDPMQLPYDSTWELPRDQ	600
Db	541	LVVLTIIISLIILIMLWQKPRYIRWKVIESVSSDGHGYIYVDPMQLPYDSTWELPRDQ	600
Qy	601	VLGRTLGSAGFGQVVEATAHGISHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP	660
Db	601	VLGRTLGSAGFGQVVEATAHGISHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP	660
Qy	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL	720
Db	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL	720
Qy	721	PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP	780
Db	721	PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP	780
Qy	781	SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Db	781	SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Qy	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Db	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Qy	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER	960
Db	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER	960
Qy	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPPLDTSSVLYTAVQPNEGDND	1020
Db	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPPLDTSSVLYTAVQPNEGDND	1020
Qy	1021	YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080
Db	1021	YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080
Qy	1081	EPEPELQPLDSCGPAPRAEAEDSFL	1106
Db	1081	EPEPELQPLDSCGPAPRAEAEDSFL	1106

RESULT 5
US-09-866-510-22
; Sequence 22, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-22

Query Match          99.9%; Score 5760; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRLPGAMPALALKGELL LLSLL LLEPQISQGLVVT PPGPELVNVSSTFVLTCSGSAPV 60
Db      1 MRLPGAMPALALKGELL LLSLL LLEPQISQGLVVT PPGPELVNVSSTFVLTCSGSAPV 60

Qy      61 VWERMSQEPPOEMAKAQDGT FSSVLT LTNLTGLD TGEYFCTHNSRGLETDERKRLYIFV 120
Db      61 VWERMSQEPPOEMAKAQDGT FSSVLT LTNLTGLD TGEYFCTHNSRGLETDERKRLYIFV 120

Qy      121 PDPTVGF L PND A EELFIFL TEIT EITIPCRVTD PQLVVT LHEKKG DVALPV PYDHQGF S 180
Db      121 PDPTVGF L PND A EELFIFL TEIT EITIPCRVTD PQLVVT LHEKKG DVALPV PYDHQGF S 180

Qy      181 GIFEDRSYICKTTIGDREVSDAYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db      181 GIFEDRSYICKTTIGDREVSDAYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Qy      241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELED SGTYTCNVTESVNDH 300
Db      241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELED SGTYTCNVTESVNDH 300

Qy      301 QDEKAINITVVESGYVRLGEGVT LQFAELHRSRTLQVVF EAYPPPTVLWFKDNR TLGDS 360
Db      301 QDEKAINITVVESGYVRLGEGVT LQFAELHRSRTLQVVF EAYPPPTVLWFKDNR TLGDS 360

Qy      361 SAGEIALSTRNVSETRYVSEL TLVRVKVAEAGHYTMRAF HEDAEVQLS FQLQINVPVRVL 420
Db      361 SAGEIALSTRNVSETRYVSEL TLVRVKVAEAGHYTMRAF HEDAEVQLS FQLQINVPVRVL 420

Qy      421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
Db      421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480

Qy      481 TYWEEEQEFVSTLRLQHVDRPLSVRCTL RNAGQDTEQVIYVPHSLPFKVVVISAILA 540
Db      481 TYWEEEQEFVSTLRLQHVDRPLSVRCTL RNAGQDTEQVIYVPHSLPFKVVVISAILA 540

Qy      541 LVVLTIIISLIILIMLWQKKPRY EIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db      541 LVVLTIIISLIILIMLWQKKPRY EIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600

Qy      601 VLGRITLGS GAFQGVVEATAHGLSHSQATMKVAVKMLKSTAR SSEKQALMSELKIMSHLGP 660
Db      601 VLGRITLGS GAFQGVVEATAHGLSHSQATMKVAVKMLKSTAR SSEKQALMSELKIMSHLGP 660

Qy      661 HLNVNLLGACTKG GPYIIT EYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL 720
Db      661 HLNVNLLGACTKG GPYIIT EYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL 720

Qy      721 PVGLPLSHVSLTGESDGGYMDSKDESVDYVPM LDMKGDVKYADI ESSNYMAPYDNYVP 780
Db      721 PVGLPLSHVSLTGESDGGYMDSKDESVDYVPM LDMKGDVKYADI ESSNYMAPYDNYVP 780

Qy      781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db      781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
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Qy      841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTT LSDVWSFGILLWEIFTLG 900
Db      841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTT LSDVWSFGILLWEIFTLG 900

Qy      901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db      901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960

Qy      961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLP GFHGLRSP LDTSSVLYTAVQPNEGND 1020
Db      961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLP GFHGLRSP LDTSSVLYTAVQPNEGND 1020

Qy      1021 YIIPDPKP E VAD EGP L E GSP S L A S S T L N E V N T S T I S C D S P L E P Q D E P E P Q L E L Q V 1080
Db      1021 YIIPDPKP E VAD EGP L E GSP S L A S S T L N E V N T S T I S C D S P L E P Q D E P E P Q L E L Q V 1080

Qy      1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db      1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 6
US-09-866-510-16
; Sequence 16, Application US/098666510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-16

Query Match          99.9%; Score 5758; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 6.2e-318;
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRLPGAMPALALKGELL LLSLL LLEPQISQGLVVT PPGPELVNVSSTFVLTCSGSAPV 60
Db      1 MRLPGAMPALALKGELL LLSLL LLEPQISQGLVVT PPGPELVNVSSTFVLTCSGSAPV 60

Qy      61 VWERMSQEPPOEMAKAQDGT FSSVLT LTNLTGLD TGEYFCTHNSRGLETDERKRLYIFV 120
Db      61 VWERMSQEPPOEMAKAQDGT FSSVLT LTNLTGLD TGEYFCTHNSRGLETDERKRLYIFV 120

Qy      121 PDPTVGF L PND A EELFIFL TEIT EITIPCRVTD PQLVVT LHEKKG DVALPV PYDHQGF S 180
Db      121 PDPTVGF L PND A EELFIFL TEIT EITIPCRVTD PQLVVT LHEKKG DVALPV PYDHQGF S 180

Qy      181 GIFEDRSYICKTTIGDREVSDAYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db      181 GIFEDRSYICKTTIGDREVSDAYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Qy      241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELED SGTYTCNVTESVNDH 300
Db      241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELED SGTYTCNVTESVNDH 300

Qy      301 QDEKAINITVVESGYVRLGEGVT LQFAELHRSRTLQVVF EAYPPPTVLWFKDNR TLGDS 360
Db      301 QDEKAINITVVESGYVRLGEGVT LQFAELHRSRTLQVVF EAYPPPTVLWFKDNR TLGDS 360

Qy      361 SAGEIALSTRNVSETRYVSEL TLVRVKVAEAGHYTMRAF HEDAEVQLS FQLQINVPVRVL 420
```

Db 361 SAGEIALSTRNVSETRVSELTILVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Qy 421 ELSESHPDGEGTQVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSESHPDGEGTQVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Qy 481 TYWEEEOQFEVWSTLRLOHVDRPLSVRCTLRNAVQDQTEVIYVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOQFEVWSTLRLOHVDRPLSVRCTLRNAVQDQTEVIYVPHSLPFKVVVISAILA 540
Qy 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFGQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSDYVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSDYVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTILSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTILSDVWSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Qy 1021 YIIPLDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Qy 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 7
US-09-866-510-20
; Sequence 20, Application US/09866510
; Patent No. US2002011304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-866-510-20
Query Match 99.8%; Score 5757; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 6.2e-318;
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MR LPGAMPALALKGELLILLSLILLLLEPQISQGLVVTTPGPELVLVNVSSTFVLTCSGSAPV 60
Db 1 MR LPGAMPALALKGELLILLSLILLLLEPQISQGLVVTTPGPELVLVNVSSTFVLTCSGSAPV 60
Qy 61 VWERMSQEPPOEMAKAQDGTFFSVLTITNLITGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTFFSVLTITNLITGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
Qy 121 PDPTVGFPLPNDAAELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVPYDHQRGFS 180
Db 121 PDPTVGFPLPNDAAELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVPYDHQRGFS 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Qy 241 DVVNFETWYPRKESGRLEVPVTDFLDMPYHIRSILHIPSALAEDESGTYTCNVTESVNDH 300
Db 241 EVVNFETWYPRKESGRLEVPVTDFLDMPYHIRSILHIPSALAEDESGTYTCNVTESVNDH 300
Qy 301 QDEKAINITVVESGYVRLLEGEVGTIQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITVVESGYVRLLEGEVGTIQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD 360
Qy 361 SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Qy 421 ELSESHPDGEGTQVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSESHPDGEGTQVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Qy 481 TYWEEEOQFEVWSTLRLOHVDRPLSVRCTLRNAVQDQTEVIYVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOQFEVWSTLRLOHVDRPLSVRCTLRNAVQDQTEVIYVPHSLPFKVVVISAILA 540
Qy 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFGQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSDYVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSDYVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTILSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTILSDVWSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020

Qy	1021	YIIPLDPKPKEVADEGPLEGSPSLASSTTLNEVNTSSTISCDSPLEQDEPEPEQLEQV	1080
Db	1021	YIIPLDPKPKEVADEGPLEGSPSLASSTTLNEVNTSSTISCDSPLEQDEPEPEQLEQV	1080
Qy	1081	EPEPELEQLPDSGCPAPRAEAEDSFL	1106
Db	1081	EPEPELEQLPDSGCPAPRAEAEDSFL	1106

RESULT 8
US-09-866-510-18
; Sequence 18, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-18

Query Match 99.8%; Score 5756; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 6.2e-318;
Matches 1104; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVWTPPGPELVNVSSFVLTCSGSAPV	60
Db	1	MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVWTPPGPELVNVSSFVLTCSGSAPV	60
QY	61	VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTGTDGTYFCTHNDSRGLTDERKRLYIFV	120
Db	61	VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTGTDGTYFCTHNDSRGLTDERKRLYIFV	120
QY	121	PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDLPQVVLHHEKKGDVALPVPYDHQGRFS	180
Db	121	PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDLPQVVLHHEKKGDVALPVPYDHQGRFS	180
QY	181	GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Db	181	GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
QY	241	DVNVFEWTPYPRKESGRVLEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH	300
Db	241	EVNVFEWTPYPRKESGRVLEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH	300
QY	301	QDEKAINITTVESGYVRLGGEVGTLOFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD	360
Db	301	QDEKAINITTVESGYVRLGGEVGTLOFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD	360
QY	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL	420
Db	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL	420
QY	421	ELSESHPDSSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTTLGNSSEESQLETNV	480
Db	421	ELSESHPDSSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTTLGNSSEESQLETNV	480
QY	481	TYWEEEEEFEVWSTLRLQHVDRPLSVRCTLRNNAVGDQTQEVIVVPHSLPFKVVVISAILA	540
Db	481	TYWEEEEEFEVWSTLRLQHVDRPLSVRCTLRNNAVGDQTQEVIVVPHSLPFKVVVISAILA	540

QY	541	LWVLTII	SLII	ILIMLWQKKPRYEIRWKVIESVSSD	GHEYIYVDPMQLPYDSTWELPRDQL	600	
Db	541	LWVLTII	SLII	ILIMLWQKKPRYEIRWKVIESVSSD	GHEYIYVDPMQLPYDSTWELPRDQL	600	
QY	601	VLGRTL	GSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTAR	SEKQALMSELKIMSHLGP	660		
Db	601	VLGRTL	GSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTAR	SEKQALMSELKIMSHLGP	660		
QY	661	HLNVN	LLGACTKGGPIYII	TEYCRYGDLVDYLHRNKHTFLOHHS	DKRRPPSAELYSNAL	720	
Db	661	HLNVN	LLGACTKGGPIYII	TEYCRYGDLVDYLHRNKHTFLOHHS	DKRRPPSAELYSNAL	720	
QY	721	PVGLPL	PSHVSLTGESDGGYMDMSKDESVDYVPM	LDKMGDVKYADIESSNYMAPYDNYVP	780		
Db	721	PVGLPL	PSHVSLTGESDGGYMDMSKDESVDYVPM	LDKMGDVKYADIESSNYMAPYDNYVP	780		
QY	781	SAPERT	CRATLINESPVL	SYMDLVGFSYQVANGMEFLASKNCVHRDLAARN	VLI	CEGKLV	840
Db	781	SAPERT	CRATLINESPVL	SYMDLVGFSYQVANGMEFLASKNCVHRDLAARN	VLI	CEGKLV	840
QY	841	KICDF	GLARDIMRDSNYISK	GSTFLPLKWMAPESIFNSLYTTLS	DVWSEFGILLWEIFTLG	900	
Db	841	KICDF	GLARDIMRDSNYISK	GSTFLPLKWMAPESIFNSLYTTLS	DVWSEFGILLWEIFTLG	900	
QY	901	GTPYPE	LPNMQFYNAIKRGYRMAQPAHASDEIYEIMQ	KWEEKFEIRPPFSQVLVLLER	960		
Db	901	GTPYPE	LPNMQFYNAIKRGYRMAQPAHASDEIYEIMQ	KWEEKFEIRPPFSQVLVLLER	960		
QY	961	LLGEGY	KKKYQQVDEEFLRSDHPAILRSQARLPGF	HGLRSP	LDTSSVLYTAVQNEGDND	1020	
Db	961	LLGEGY	KKKYQQVDEEFLRSDHPAILRSQARLPGF	HGLRSP	LDTSSVLYTAVQNEGDND	1020	
QY	1021	YIIP	LPDPKPEVADEGP	LEGSPSLASSTLNEVNTSSTISCDSPLE	QDEPEPEQLELOV	1080	
Db	1021	YIIP	LPDPKPEVADEGP	LEGSPSLASSTLNEVNTSSTISCDSPLE	QDEPEPEPEQLELOV	1080	
QY	1081	EPEPE	LEQLPDSGCCPAPRAEADSFL	1106			
Db	1081	EPEPE	LEQLPDSGCCPAPRAEADSFL	1106			

RESULT 9
 US-09-866-510-14
 ; Sequence 14, Application US/09866510
 ; Patent No. US20020111304A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KAZLAUSKAS, ANDRIUS
 ; APPLICANT: IKUNO, YASUSHI
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
 ; FILE REFERENCE: ERM-104.01
 ; CURRENT APPLICATION NUMBER: US/09/866,510
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/250,747
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: 60/289,103
 ; PRIOR FILING DATE: 2001-05-07
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 1090
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-866-510-14

Query Match	98.4%	Score 5676;	DB 9;	Length 1090;
Best Local Similarity	99.9%;	Pred. NO. 1.4e-313;		
Matches 1089; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MRLPGAMPALAKGELL	LL	LLLL	LEPQISQGLVVT	PP	GPELV	LV	NV	SV	TF	VL	TC	SG	SA	PV	60																	
QY																																		
Db	1	MRLPGAMPALAKGELL <th>LL</th> <th>LLLL</th> <th>LEPQISQGLVVT</th> <th>PP</th> <th>GPELV</th> <th>LV</th> <th>NV</th> <th>SV</th> <th>TF</th> <th>VL</th> <th>TC</th> <th>SG</th> <th>SA</th> <th>PV</th> <th>60</th>	LL	LLLL	LEPQISQGLVVT	PP	GPELV	LV	NV	SV	TF	VL	TC	SG	SA	PV	60																	
QY	61	VWERM	SOEPP	QPM	AKAQD	GT	FSS	VLT	LT	LT	LT	GL	DT	GEY	F	CT	HN	DS	R	G	L	E	T	D	E	R	K	R	L	Y	I	F	V	12

Db 61 VWERMSQEPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVYDHQRGFS 180
Db 121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVYDHQRGFS 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNPFWTYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSVNDH 300
Db 241 EVNPFWTYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSVNDH 300
QY 301 QDEKAINITVVEGSGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGD 360
Db 301 QDEKAINITVVEGSGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIISACRDLKRCPRELPPILLGNSSEESQLETVN 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIISACRDLKRCPRELPPILLGNSSEESQLETVN 480
QY 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKKPR 561
Db 541 LVVLTIIISLIILMLWQKKPR 561
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSSELKIMSHLGP 660
QY 661 HLNVNVLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHSDDKRRPPSAEALYSNAL 720
Db 661 HLNVNVLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHSDDKRRPPSAEALYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDSKDESVDYVPM LDKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSVDWMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSVDWMSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLP 1090
Db 1081 EPEPELEQLP 1090

RESULT 10

US-09-866-510-24
; Sequence 24, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-24

Query Match 50.0%; Score 2882; DB 9; Length 561;
Best Local Similarity 99.8%; Pred. No. 2.2e-155;
Matches 560; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVTPPGPELVLVNSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVTPPGPELVLVNSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVYDHQRGFS 180
Db 121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALPVYDHQRGFS 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNPFWTYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSVNDH 300
Db 241 EVNPFWTYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSVNDH 300
QY 301 QDEKAINITVVEGSGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGD 360
Db 301 QDEKAINITVVEGSGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIISACRDLKRCPRELPPILLGNSSEESQLETVN 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIISACRDLKRCPRELPPILLGNSSEESQLETVN 480
QY 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKKPR 561
Db 541 LVVLTIIISLIILMLWQKKPR 561

RESULT 11
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS

Db 122 PDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTETPTLHNSEG--VVPASYDSRQGFN 179
QY 181 GIFEDRSYICKTTIGDREVSDDAYVYVRLQVSS-INVSNAVQTVVRQGENITLMCIVIG 239
Db 180 GTFTVGPIYCEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
QY 240 NDVNVFEWTPRKESGR--LVEPVTDFLLDMPYHIRSILHIPSAAELSDSGTYTCNVTES 296
Db 240 NEVVDLQWTPGEGVKGKITMLEEIKVPSIKLVY---TLTVPEATVKDSGDYECARQA 295
QY 297 VNDHQDEKAINITVVEGYVRLGEGVGTLOFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356
Db 296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
QY 357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416
Db 356 LIENLT-EITTDVEKIQEIRYRSKCLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
QY 417 VRVLELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNS----- 469
Db 415 SSILDVLDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIIT 474
QY 470 ---SEESQLETNVTYWEEEQEFVVSTLRLQHVDRLPSVRCTLRNAVQDQTQEVIVVPH 526
Db 475 EIHSRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVAP 519
QY 527 SLPFKVVVISAILALVLTIIISLIILIMLWQKPPRYEIRWKVIESVSSDGHEYIYVDPMQ 586
Db 520 TLRSELTVAAAVLLVIVIIISLIVVVIWKQPRYEURWRVIESISPDGHEYIYVDPMQ 579
QY 587 LPYDSTWELPRDQLVGLRGLSGAFGVVEBATAHGLSHSQATMKVAVKMLKSTARSEKQ 646
Db 580 LPYDSRWEFPRDGLVLRVGLSGAFGVVEGTAYGLSRSQPVMKVAVKMLKPTARSEKQ 639
QY 647 ALMSELKIMSHLGPHLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSD 706
Db 640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDVLNVLHKNRDSFLSHPE 699
QY 707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPM LDKMGDVKYAD 765
Db 700 K--PKKELDTFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLEKREVSKYSYD 756
QY 766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824
Db 757 IORSLYDRPASYKKKSM LDDSEVKNLLSDNSEGLTLDDLSTFYQVARGMEFLASKNCVH 816
QY 825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWNAPESIFNSLYTTLS 884
Db 817 RDLAARNVLLAQQKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWNAPESIFDNLYTTLS 876
QY 885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944
Db 877 DVWSYGILLWEIFSLGGTPYPGMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
QY 945 FEIRPPFSQLVLLERLLGEGYKKYQQVDEEFRLSDHPAILRSQARLPGFHGLRSPLDT 1004
Db 937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----VDS 984
QY 1005 SSVLYTAVQPNE-----GDNDYIIPLP--DPKPEVADEGLEGPSLA 1045
Db 985 DNAYIGVTYKNEEDKLDWEGGLDEQRLSADSGYIIPLPDIDPVEEEDLGKRNHRHSQT 1044
QY 1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELOVEPEPELEQLPDSGCCPAPRAEAD 1103
Db 1045 SEESAIEGSSSSTF-----IKREDE-----TIE---DIDMDDDIGDSSDL-VED 1086
QY 1104 SFL 1106
Db 1087 SFL 1089

US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-90

Query Match 40.8%; Score 2351.5; DB 9; Length 1089;
Best Local Similarity 44.0%; Pred.No. 6.4e-125;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

QY 8 PALALKGELLL-LSLLLLLEPQISQGLVVTTPGPELVLVNSFTVLTCSGSAPVWVE-RM 65
Db 6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVQVQLNSSFSRLCFGESEVSWQYPM 61
QY 66 SQEPPQEM----AKAQDGTFSVLTLTNLTLGLDTGEYFCTHNSDRGLETD-ERKRLYIFV 120
Db 62 SEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTEENELEGRHIYIV 121
QY 121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVTLHEKKGDVLPVPYDHQRGFS 180
Db 122 PDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTETPTLHNSEG--VVPASYDSRQGFN 179
QY 181 GIFEDRSYICKTTIGDREVSDDAYVYVRLQVSS-INVSNAVQTVVRQGENITLMCIVIG 239
Db 180 GTFTVGPIYCEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
QY 240 NDVNVFEWTPRKESGR--LVEPVTDFLLDMPYHIRSILHIPSAAELSDSGTYTCNVTES 296
Db 240 NEVVDLQWTPGEGVKGKITMLEEIKVPSIKLVY---TLTVPEATVKDSGDYECARQA 295
QY 297 VNDHQDEKAINITVVEGYVRLGEGVGTLOFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356
Db 296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
QY 357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416
Db 356 LIENLT-EITTDVEKIQEIRYRSKCLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
QY 417 VRVLELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNS----- 469
Db 415 SSILDVLDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIIT 474
QY 470 ---SEESQLETNVTYWEEEQEFVVSTLRLQHVDRLPSVRCTLRNAVQDQTQEVIVVPH 526
Db 475 EIHSRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVAP 519
QY 527 SLPFKVVVISAILALVLTIIISLIILIMLWQKPPRYEIRWKVIESVSSDGHEYIYVDPMQ 586
Db 520 TLRSELTVAAAVLLVIVIIISLIVVVIWKQPRYEURWRVIESISPDGHEYIYVDPMQ 579
QY 587 LPYDSTWELPRDQLVGLRGLSGAFGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQ 646
Db 580 LPYDSRWEFPRDGLVLRVGLSGAFGVVEGTAYGLSRSQPVMKVAVKMLKPTARSEKQ 639
QY 647 ALMSELKIMSHLGPHLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSD 706
Db 640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDVLNVLHKNRDSFLSHPE 699
QY 707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPM LDKMGDVKYAD 765

Db	700	K----	PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLEKVESKYS	756
Qy	766	IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGSYQVANGMEFLASKNCVH	824	
Db	757	IQRSLYDRPASYYKKKMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH	816	
Qy	825	RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS	884	
Db	817	RDLAARNVLLAOGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTL	876	
Qy	885	DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK	944	
Db	877	DVWSYGILLWEIFSLGGTPYPGMVVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE	936	
Qy	945	FEIRPPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT	1004	
Db	937	PEKRPSFYHLSEIVENLLPGQYKSYEKIHLDFLKSDHPAVARMR-----VDS	984	
Qy	1005	SSVLYTAVQPNE-----GNDYIILPL--DPKPEVADEGPLEGSPSLA	1045	
Db	985	DNAYIGVTKNEEDKLDKWEGLDEQRLSADSGYIILPDIDPVPEEEDLGKRNHSSQT	1044	
Qy	1046	S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELBQLPDSCGCPAPRAEAE	1103	
Db	1045	SEESALETGSSSSTF-----IKREDE-----TIE---DIDMDDIGDSSDL-VED	1086	
Qy	1104	SFL 1106		
Db	1087	SFL 1089		
RESULT 14				
US-09-866-510-2				
; Sequence 2, Application US/09866510				
; Patent No. US2002011304A1				
; GENERAL INFORMATION:				
; APPLICANT: KAZLAUSKAS, ANDRIUS				
; APPLICANT: IKUNO, YASUSHI				
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES				
; FILE REFERENCE: ERM-104.01				
; CURRENT APPLICATION NUMBER: US/09/866,510				
; CURRENT FILING DATE: 2001-05-25				
; PRIOR APPLICATION NUMBER: 60/250,747				
; PRIOR FILING DATE: 2000-12-01				
; PRIOR APPLICATION NUMBER: 60/289,103				
; PRIOR FILING DATE: 2001-05-07				
; NUMBER OF SEQ ID NOS: 33				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 2				
; LENGTH: 1089				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-09-866-510-2				
Query Match 40.8%; Score 2351.5; DB 9; Length 1089;				
Best Local Similarity 44.0%; Pred. No. 6.4e-125;				
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;				
Qy	8	PALALKGELL-LSLLLLEPQISQGLVVTPPGPELVNVSSTFVLTCGSA PVVWE-RM	65	
Db	6	PAFLVLGCLLTGLSLILC--QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM	61	
Qy	66	SQEPPEM-----AKAQDGTFSFVLTTLNLTGLDGTGEYFCTHNDNRGLSTD-ERKRLYIFV	120	
Db	62	SEESSDVEIRNEENNSGLFVTVLVSVSSASAHTGLTYCYNNHTQTEENELEGRHIYIV	121	
Qy	121	PDPTVGLPNDABELFIFLTEITEITIPCRVTDPLQVLTLHEKKGDVALPVPYDHORGFS	180	
Db	122	PDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDTPETPVILHNSG--VVPASYDSRQGFN	179	
Qy	181	GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSS-INVSNAVQTVVRQGENITLMCIVIG	239	
Db	180	GTFTVGYPYICATVKGKKFQTIPIPNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN	239	

Qy	240	NDVVNFEWTPYRKESGR---LVEPVTDFTDLDMPYHIRSILHIPSAELEDSTGYTCNVTES	296
Db	240	NEVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVY---TLTVPEATVKDSDGYECAARQA	295
Qy	297	VNDHQDEKAINITVVESGYVRLGEGVGTQLQFAELHRSRTLQVVFVFEAYPPPTVLWFKDNRT	356
Db	296	TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT	355
Qy	357	LGDSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAELVLSFQLQINVP	416
Db	356	LIENLT-EITDVEKIQEIRVRSKLLIRAKEEDSGHYTTIVAQNEDAVKSYTFELLTQVP	414
Qy	417	VRVLELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNS-----	469
Db	415	SSILDVLDDHHGSTGGQTVRCTAEGTLPDIEWMICKDIKCNNETSWTILANNVSNIT	474
Qy	470	---SEESQLETNVTYWEEOEFVSVTLRQLQHVDRPLSVRCTLRNAVQDQTEVIVVPH	526
Db	475	EIHSRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVAP	519
Qy	527	SLPFKVVVISAILALVLTIIISLIILMLWQKPPRYEIRWKVIESVSSDGHEYIYVDPMQ	586
Db	520	TLRSELTVAAAVLVIVIIISLIVLVIVWKQPRYEIRWRVIESISPDGHEYIYVDPMQ	579
Qy	587	LPYDSTWELPRDQLVLGRTLGSGAFGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQ	646
Db	580	LPYDSRWEFPRDGLVLGRVLGSGAFGVVEGTAYGLSRSQPMKVAVKMLKPTARSSEKQ	639
Qy	647	ALMSELKIMSHLGPLNVLNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD	706
Db	640	ALMSELKIMTHLGPLNVLNLLGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPE	699
Qy	707	KRRPESAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYAD	765
Db	700	K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLEKVESKYS	756
Qy	766	IESNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGSYQVANGMEFLASKNCVH	824
Db	757	IQRSLYDRPASYYKKKMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH	816
Qy	825	RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS	884
Db	817	RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTLS	876
Qy	885	DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEK	944
Db	877	DVWSYGILLWEIFSLGGTPYPGMVVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE	936
Qy	945	FEIRPPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT	1004
Db	937	PEKRPSFHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----VDS	984
Qy	1005	SSVLYTAVQPNE-----GNDYIILPL--DPKPEVADEGPLEGSPSLA	1045
Db	985	DNAYIGVTKNEEDKLDKOWEGLDEQRLSADSGYIILPDIDPVPEEEDLGKRNHSSQT	1044
Qy	1046	S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELBQLPDSCGCPAPRAEAD	1103
Db	1045	SEESALETGSSSSTF-----IKREDE-----TIE---DIDMDDIGIDSSDL-VED	1086
Qy	1104	SFL 1106	
Db	1087	SFL 1089	
RESULT 15			
US-09-955-363-36			
; Sequence 36, Application US/099555363			
; Patent No. US20020173621A1			
; GENERAL INFORMATION:			
; APPLICANT: Sledziowski Ph.D., Andrzej Z			
; Bell, Lillian A.			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:10:35 ; Search time 32.2478 Seconds
(without alignments)
2560.230 Million cell updates/sec

Title: US-10-027-400-4
Perfect score: 5766
Sequence: 1 MRLPGAMPALALKGELLLS.....EQLPDGCGPAPRAEADSFL 1106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5766	100.0	1106	1 US-08-168-917-2	Sequence 2, Appli
2	5766	100.0	1106	2 US-08-460-510-2	Sequence 2, Appli
3	5766	100.0	1106	2 US-08-460-490-2	Sequence 2, Appli
4	5766	100.0	1106	3 US-08-462-728-4	Sequence 4, Appli
5	5766	100.0	1106	3 US-08-461-917-4	Sequence 4, Appli
6	5766	100.0	1106	4 US-08-464-436-4	Sequence 4, Appli
7	5766	100.0	1106	4 US-08-464-436-4	Sequence 4, Appli
8	5766	100.0	1106	5 PCT-US92-00730-2	Sequence 2, Appli
9	5766	100.0	1106	5 PCT-US92-00862-2	Sequence 2, Appli
10	5762	99.9	1106	1 US-08-180-195-2	Sequence 2, Appli
11	5762	99.9	1106	1 US-08-477-329-2	Sequence 2, Appli
12	5762	99.9	1106	2 US-08-475-458-2	Sequence 2, Appli
13	5762	99.9	1106	3 US-08-980-400-2	Sequence 2, Appli
14	5762	99.9	1106	3 US-09-583-459A-2	Sequence 2, Appli
15	5762	99.9	1106	3 US-09-583-210-2	Sequence 2, Appli
16	5762	99.9	1106	3 US-09-583-449A-2	Sequence 2, Appli
17	5762	99.9	1106	3 US-09-435-059-2	Sequence 2, Appli
18	5760	99.9	1106	4 US-09-866-510-22	Sequence 22, Appl
19	5758	99.9	1106	4 US-09-866-510-16	Sequence 16, Appl
20	5757	99.8	1106	4 US-09-866-510-20	Sequence 20, Appl
21	5756	99.8	1106	4 US-09-866-510-18	Sequence 18, Appl
22	5766	98.4	1090	4 US-09-866-510-14	Sequence 14, Appl
23	3076	53.3	668	4 US-09-949-016-8139	Sequence 8139, Ap
24	2882	50.0	561	4 US-09-866-510-24	Sequence 24, Appl
25	2675.5	46.4	566	1 US-08-810-116-11	Sequence 11, Appl
26	2675.5	46.4	566	2 US-07-930-548A-11	Sequence 11, Appl
27	2352.5	40.8	1089	4 US-09-866-510-10	Sequence 10, Appl

28	2351.5	40.8	1089	1 US-08-180-195-36	Sequence 36, Appl
29	2351.5	40.8	1089	1 US-08-168-917-4	Sequence 4, Appli
30	2351.5	40.8	1089	1 US-08-477-329-36	Sequence 36, Appl
31	2351.5	40.8	1089	2 US-08-475-458-36	Sequence 36, Appl
32	2351.5	40.8	1089	2 US-08-460-510-4	Sequence 4, Appli
33	2351.5	40.8	1089	2 US-08-460-490-4	Sequence 4, Appli
34	2351.5	40.8	1089	3 US-08-980-400-36	Sequence 36, Appl
35	2351.5	40.8	1089	3 US-08-462-728-2	Sequence 2, Appli
36	2351.5	40.8	1089	3 US-09-583-459A-36	Sequence 36, Appl
37	2351.5	40.8	1089	3 US-09-583-210-36	Sequence 36, Appl
38	2351.5	40.8	1089	3 US-09-583-449A-36	Sequence 36, Appl
39	2351.5	40.8	1089	3 US-09-435-059-36	Sequence 36, Appl
40	2351.5	40.8	1089	3 US-08-461-917-2	Sequence 2, Appli
41	2351.5	40.8	1089	4 US-08-464-436-2	Sequence 2, Appli
42	2351.5	40.8	1089	4 US-08-464-436-2	Sequence 2, Appli
43	2351.5	40.8	1089	4 US-09-769-987-2	Sequence 2, Appli
44	2351.5	40.8	1089	4 US-09-866-510-2	Sequence 2, Appli
45	2351.5	40.8	1089	4 US-09-919-497-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-08-168-917-2
; Sequence 2, Application US/08168917
; Patent No. 5686572
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-168-917-2

Query Match 100.0%; Score 5766; DB 1; Length 1106;

[illegible]

Db	1021	YIIPLPDPKPEVADEGP	LEGSP	SLASSTLN	NEVNTS	TISCDS	PLEPQDEPEPEPQ	LELQV	108
QY	1081	EPEPELEQLPDSGCPAPRAE	ADSFL	1106					
Db	1081	EPEPELEQLPDSGCPAPRAE	ADSFL	1106					
<p>RESULT 2</p> <p>US-08-460-510-2</p> <p>; Sequence 2, Application US/08460510</p> <p>; Patent No. 5872218</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Wolf, David</p> <p>; APPLICANT: Tomlinson, James E.</p> <p>; APPLICANT: Fretto, Larry J.</p> <p>; APPLICANT: Giese, Neill A.</p> <p>; APPLICANT: Escobedo, Jaime A.</p> <p>; APPLICANT: Williams, Lewis T.</p> <p>; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN</p> <p>; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES</p> <p>; NUMBER OF SEQUENCES: 23</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: TOWNSEND and TOWNSEND and CREW</p> <p>; STREET: One Market Plaza, Steuart Street Tower, Suite 2000</p> <p>; CITY: San Francisco</p> <p>; STATE: California</p> <p>; COUNTRY: US</p> <p>; ZIP: 94105</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; COMPUTER: IBM PC compatible</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/460,510</p> <p>; FILING DATE: 02-JUN-1995</p> <p>; CLASSIFICATION: 435</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Dow, Karen B.</p> <p>; REGISTRATION NUMBER: 29,684</p> <p>; REFERENCE/DOCKET NUMBER: 012418-001430</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (415) 326-2400</p> <p>; TELEFAX: (415) 326-2422</p> <p>; INFORMATION FOR SEQ ID NO: 2:</p> <p>; SEQUENCE CHARACTERISTICS:</p> <p>; LENGTH: 1106 amino acids</p> <p>; TYPE: amino acid</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: protein</p> <p>US-08-460-510-2</p> <p>Query Match 100.0%; Score 5766; DB 2; Length 1106;</p> <p>Best Local Similarity 100.0%; Pred. No. 0;</p> <p>Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>									
QY	1	MRLPGAMPALAKGELL	LLSLL	LLLEPOISQGLV	VTTPPGPELV	LVNSSTFVL	TCGSA	PV 60	
Db	1	MRLPGAMPALAKGELL	LLSLL	LLLEPOISQGLV	VTTPPGPELV	LVNSSTFVL	TCGSA	PV 60	
QY	61	VWERMSQEPQEMAKA	QDGT	FSSVLT	LTNL	TGLD	TGEY	FCTH	ND
Db	61	VWERMSQEPQEMAKA	QDGT	FSSVLT	LTNL	TGLD	TGEY	FCTH	ND
QY	121	PDPTVGFLEPNDABE	LFI	FLTEI	TEIT	PCR	VTDP	QLV	VT
Db	121	PDPTVGFLEPNDABE	LFI	FLTEI	TEIT	PCR	VTDP	QLV	VT
QY	181	GIFEDRSYICKTTIG	DRE	VSD	DAY	VYRL	QVSS	IN	SV
Db	181	GIFEDRSYICKTTIG	DRE	VSD	DAY	VYRL	QVSS	IN	SV
QY	241	DVNVFENTYPRKES	GR	LV	EP	VTDF	EL	DM	PH
Db	241	DVNVFENTYPRKES	GR	LV	EP	VTDF	EL	DM	PH

Db 241 DVNFEWTPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTYTCNVTESVNDH 300
QY 301 ODEKAINITVVEGYSYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGDS 360
Db 301 ODEKAINITVVEGYSYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNNAVGDQTEQIVVPHSLPFFKVVVISAILA 540
Db 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNNAVGDQTEQIVVPHSLPFFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLRHNKHTFLQHSKDRPPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLRHNKHTFLQHSKDRPPPSAELYSNAL 720
QY 721 PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGKLV 840
Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPKWMAPESEIFNSLYTTLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPKWMAPESEIFNSLYTTLSDVMSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVLYTAVQPNEGDND 1020
QY 1021 YIIPLDPKPEVADEGPLEGSPSLASSTILNEVNTSSTISCDSPLEQDEPEPEQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLEGSPSLASSTILNEVNTSSTISCDSPLEQDEPEPEPEQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 3
US-08-460-490-2
; Sequence 2, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES

; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-490-2

Query Match 100.0%; Score 5766; DB 2; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVWTPPGPELVNVSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVWTPPGPELVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLJETDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLJETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAAELFIFLTEITEITPCRVTDLPQLVTLHKKGDVALPVYPYDHQGRFS 180
Db 121 PDPTVGFLPNDAAELFIFLTEITEITPCRVTDLPQLVTLHKKGDVALPVYPYDHQGRFS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTYTCNVTESVNDH 300
Db 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTYTCNVTESVNDH 300
QY 301 ODEKAINITVVEGYSYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGDS 360
Db 301 ODEKAINITVVEGYSYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNNAVGDQTEQIVVPHSLPFFKVVVISAILA 540
Db 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNNAVGDQTEQIVVPHSLPFFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQL 600

Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMEQFVNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMEQFVNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPFGFHLRSPLDTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPFGFHLRSPLDTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADGPLEGSPSLASSTILNEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
Db 1021 YIIPLPDPKPEVADGPLEGSPSLASSTILNEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

RESULT 4

US-08-462-728-4
; Sequence 4, Application US/08462728
; Patent No. 6043211
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,728
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-728-4

Query Match 100.0%; Score 5766; DB 3; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALALKGELLSSLLLLLEPQISQGLVVTTPGPELVLVNVSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKGELLSSLLLLLEPQISQGLVVTTPGPELVLVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPOEMAKAQDGTFSVLTNLTLGDTGEYFCTHNSRGLTDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTNLTLGDTGEYFCTHNSRGLTDERKRLYIFV 120
QY 121 PDPTVGFLPNDAAELFIFLTEITEITPCRVTDLPQLVVTLHEKKGVALPVYPYDHQGRFS 180
Db 121 PDPTVGFLPNDAAELFIFLTEITEITPCRVTDLPQLVVTLHEKKGVALPVYPYDHQGRFS 180
QY 181 GIFEDRSYICKTTIGDREVSDSAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDSAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFETYPKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
Db 241 DVVNFETYPKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
QY 301 ODEKAINITVVESGYVRLGEGVTGLOFAELHRSRTLOVVFAYPPTVLFKDNRTLGD 360
Db 301 ODEKAINITVVESGYVRLGEGVTGLOFAELHRSRTLOVVFAYPPTVLFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
QY 481 TYWEEEQEFVWSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEQEFVWSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLDPKPEVADEGPLGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 5
US-08-461-917-4
; Sequence 4, Application US/08461917
; Patent No. 6372438
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-917-4

Query Match 100.0%; Score 5766; DB 3; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALAKGELLLSLLLEPQISQGLVVTTPGPPELVLVNSSTFVLTCSGSAPV 60
|||||

Db 1 MRLPGAMPALAKGELLLSLLLEPQISQGLVVTTPGPPELVLVNSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLGTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
|||||
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLGTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
QY 121 PDPTVGFPLNDABELFIFLTEITEITIPCRVTPQLVTLHEKKGDVALPVPYDHQRGFS 180
|||||
Db 121 PDPTVGFPLNDABELFIFLTEITEITIPCRVTPQLVTLHEKKGDVALPVPYDHQRGFS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGTYTCNVTESVNDH 300
Db 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGTYTCNVTESVNDH 300
QY 301 QDEKAINITVVEGCVVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGD 360
Db 301 QDEKAINITVVEGCVVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTVLMFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
QY 421 ELSSEHPSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTTLGNSSEESQLETNV 480
Db 421 ELSSEHPSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTTLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVWVSTLRLOHVDRPLSVRCTLRNAVGDQTQEVIVVPHSIPFKVVVISAILA 540
Db 481 TYWEEEOEFVWVSTLRLOHVDRPLSVRCTLRNAVGDQTQEVIVVPHSIPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGEIYVDDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGEIYVDDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVMLKSTARSSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVMLKSTARSSSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLYHRNKHTFLQHHSDKRRPPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLYHRNKHTFLQHHSDKRRPPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDSKDESVDYVPMDDMKDGVKADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDSKDESVDYVPMDDMKDGVKADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSDVGVSYQVANGMEFLASKNCVHRDLAARNVLIPEGKLV 840
Db 781 SAPERTCRATLINESPVLSDVGVSYQVANGMEFLASKNCVHRDLAARNVLIPEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLDPKPEVADEGPLGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLGSPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 6
US-08-464-436-4
; Sequence 4, Application US/08464436
; Patent No. 6514723
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,436
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-436-4

Query Match 100.0%; Score 5766; DB 4; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALAKGELLALLSLLLEPQISQGLVVTTPGPELVNVSTFVLTCSGSAPV 60
DQ 1 MRLPGAMPALAKGELLALLSLLLEPQISQGLVVTTPGPELVNVSTFVLTCSGSAPV 60
QY 61 VWERMSQEPQEMAKAQDGTFSVLTTLNLTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
DQ 61 VWERMSQEPQEMAKAQDGTFSVLTTLNLTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
QY 121 PDPTVGFLPNDABELFIFLITEITIPCRVTDQQLVTLHEKGDVALPVPYDHQGF 180
DQ 121 PDPTVGFLPNDABELFIFLITEITIPCRVTDQQLVTLHEKGDVALPVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
DQ 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNFEWTPRKESGRLEVPVTDVFLDMPYHRSILHIPSALAEEDSGTYTCNVTESVNDH 300
DQ 241 DVNFEWTPRKESGRLEVPVTDVFLDMPYHRSILHIPSALAEEDSGTYTCNVTESVNDH 300
QY 301 QDEKAINITVVEGYSVRLLEGEVGTLOQFAELHRSRTLOQVFEAYPPTVLFKDNRTLGDS 360

Db 301 QDEKAINITVVEGYSVRLLEGEVGTLOQFAELHRSRTLOQVFEAYPPTVLFKDNRTLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGAGHYTMRAFHEAEVQLSFOLQINVPVRVL 420
DQ 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGAGHYTMRAFHEAEVQLSFOLQINVPVRVL 420
QY 421 ELSHSDPSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
DQ 421 ELSHSDPSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
QY 481 TYWEEQEFVSTLRLOHVDRPLSVRCTLRNAGVQDTQEVIVVPHSLPFKVVVISAILA 540
DQ 481 TYWEEQEFVSTLRLOHVDRPLSVRCTLRNAGVQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHGHIYVDPMLPYDSTWELPRDQL 600
DQ 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHGHIYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
DQ 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHHSKRRPPSAEALYSNAL 720
DQ 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHHSKRRPPSAEALYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGYMDMSKDESVDYVPMMDKGVKYADIENSNMAYPDNYVP 780
DQ 721 PVGLPLPSHVSLTGESDGYMDMSKDESVDYVPMMDKGVKYADIENSNMAYPDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
DQ 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKSTFPLPKWMAPESEIFNSLYTTLSDVMSFGILLWEIFTLG 900
DQ 841 KICDFGLARDIMRDSNYISKSTFPLPKWMAPESEIFNSLYTTLSDVMSFGILLWEIFTLG 900
QY 901 GTPYELPMNEQFYNAIKRGYNAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER 960
DQ 901 GTPYELPMNEQFYNAIKRGYNAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSHPAILRSQARLPFGHGLRSLDTSVLYTAVQPNEGDND 1020
DQ 961 LLGEGYKKYQQVDEEFLRSHPAILRSQARLPFGHGLRSLDTSVLYTAVQPNEGDND 1020
QY 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
DQ 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
QY 1081 EPEPELQLPDSCGAPRAEADSFL 1106
DQ 1081 EPEPELQLPDSCGAPRAEADSFL 1106

RESULT 7
US-08-464-436-4
; Sequence 4, Application US/08464436
; Patent No. 6642022
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,436
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-464-436-4

Query Match 100.0%; Score 5766; DB 4; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLPGAMPALALKGELLSSLLLEPQISQGLVWTPPGPELVNVSSSTFVLTCGSAVP 60
Db 1 MRLPGAMPALALKGELLSSLLLEPQISQGLVWTPPGPELVNVSSSTFVLTCGSAVP 60
Qy 61 VWERMSQEPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
Db 61 VWERMSQEPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
Qy 121 PDPTVGFLPNDABELFIFLTFITCRVTDLPQVLTLEKKGVALPVPYDHQGF 180
Db 121 PDPTVGFLPNDABELFIFLTFITCRVTDLPQVLTLEKKGVALPVPYDHQGF 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Qy 241 DVNFEWTPYRKESGRLEVPVTDFLDMPYHRSILHIPSALAEDESGTYTCNVTVSNDH 300
Db 241 DVNFEWTPYRKESGRLEVPVTDFLDMPYHRSILHIPSALAEDESGTYTCNVTVSNDH 300
Qy 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGD 360
Db 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLLVRVKVAEGHYTMRAFHEAEVLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLLVRVKVAEGHYTMRAFHEAEVLSFQLQINVPVRVL 420
Qy 421 ELSHSDPSGEQTVRCRGRMPQPNIIWSACRDLKRCRPRELPPILLGNSSSEESQLETNV 480
Db 421 ELSHSDPSGEQTVRCRGRMPQPNIIWSACRDLKRCRPRELPPILLGNSSSEESQLETNV 480
Qy 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAGQDTQEVIVVPHSLPFFKVVVISAILA 540
Db 481 TYWEEEQEFVSTLRLQHVDRPLSVRCTLRNAGQDTQEVIVVPHSLPFFKVVVISAILA 540
Qy 541 LVVLTIIISLIIIMLWQKPRYERIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIIIMLWQKPRYERIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600

Qy 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRNKHHTFLQHSKRRPPPSAEALYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRNKHHTFLQHSKRRPPPSAEALYSNAL 720
Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLGYFSYQVANGMEFLASKNCVHRDLAARNVLIPEGKLV 840
Db 781 SAPERTCRATLINESPVLGYFSYQVANGMEFLASKNCVHRDLAARNVLIPEGKLV 840
Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960
Qy 961 LLGEGYKKYQQVDEEFLRSDHPALRSQARLPFGHGLRSPDLTSSVLYTAVQPNEGND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPALRSQARLPFGHGLRSPDLTSSVLYTAVQPNEGND 1020
Qy 1021 YIIPLDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Qy 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 8

; Sequence 2, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00730
; FILING DATE: 19920128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400

QY 121 PDPTVGLPNDABELFIFLTFEITIPCRVTDPLQVWTLHEKKGDVALPVPYDHQGF 180
Db 121 PDPTVGLPNDABELFIFLTFEITIPCRVTDPLQVWTLHEKKGDVALPVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTIVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTIVRQGENITLMCIVIGN 240
QY 241 DVNFEWTFYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTGTYTCNVTVESVNDH 300
Db 241 DVNFEWTFYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTGTYTCNVTVESVNDH 300
QY 301 QDEKAINITVVEGVRLLGEVGTLOFAELHRSRTLOVFEAYPPPTVLMFKDNRTLGD 360
Db 301 QDEKAINITVVEGVRLLGEVGTLOFAELHRSRTLOVFEAYPPPTVLMFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLRVKVABAGHYTMRAFHEDEAVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLRVKVABAGHYTMRAFHEDEAVQLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEOTVRCRGRGMPQPNIIWSACRDLKRCRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEOTVRCRGRGMPQPNIIWSACRDLKRCRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLOHVDRPLSVRCITLRNAVQDQTOEIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLOHVDRPLSVRCITLRNAVQDQTOEIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLQPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLQPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVAVNLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Db 661 HLNVAVNLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMGDKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMGDKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWNAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWNAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEQLELQV 1080
Db 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

RESULT 10.
US-08-180-195-2
; Sequence 2, Application US/08180195

; Patent No. 5567584
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,195
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,510
; FILING DATE:
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-180-195-2

Query Match 99.9%; Score 5762; DB 1; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRLPGAMPALALKGELLALLSLLLEPOISQGLVWTPPGPELVLVNVSFVLTCSGSAPV 60
QY 61 VWERMSQEPPEQEMAKAQDGTFSVLTNLTLGLDTGEYFCTHNDSRGLTDERKRLYIFV 120
Db 61 VWERMSQEPPEQEMAKAQDGTFSVLTNLTLGLDTGEYFCTHNDSRGLTDERKRLYIFV 120
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Db 121 PDPTVGLPNDABELFIFLTFEITIPCRVTDPLQVWTLHEKKGDVALPVPYDHQGF 180
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Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTIVRQGENITLMCIVIGN 240
QY 241 DVNFEWTFYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTGTYTCNVTVESVNDH 300
Db 241 EVNFEWTFYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAAELEDSTGTYTCNVTVESVNDH 300

QY 301 QDEKAINITVVESGYVRLGVEVGTLLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITVVESGYVRLGVEVGTLLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSDYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
Db 781 SAPERTCRATLINESPVLSDYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWNAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWNAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLDPKPEVADEGPLEGSPSLASSTINEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLEGSPSLASSTINEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

RESULT 11
US-08-477-329-2
; Sequence 2, Application US/08477329
; Patent No. 5750375
; GENERAL INFORMATION:
; APPLICANT: Sledziowski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,329
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-329-2

Query Match 99.9%; Score 5762; DB 1; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALALKCELLLSLLLEPPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKCELLLSLLLEPPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQPPQEMAKAODGTFSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Db 61 VWERMSQPPQEMAKAODGTFSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
QY 121 PDPTVGLPNDABELFIFLTEITEITPCRVTDLPQLVVTLHEKKGDVALVPYDHQGF 180
Db 121 PDPTVGLPNDABELFIFLTEITEITPCRVTDLPQLVVTLHEKKGDVALVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINSVNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINSVNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
Db 241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
QY 301 QDEKAINITVVESGYVRLGVEVGTLLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITVVESGYVRLGVEVGTLLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHGHEIYIYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660

QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHS DKRRPPSAE LYSNAL 720
| | | | |
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHS DKRRPPSAE LYSNAL 720
| | | | |
QY 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
| | | | |
Db 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
| | | | |
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
| | | | |
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
| | | | |
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
| | | | |
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
| | | | |
QY 901 GTPYPELPMNEOFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
| | | | |
Db 901 GTPYPELPMNEOFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
| | | | |
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSP LDTSSVLYTAVQPNEGDND 1020
| | | | |
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSP LDTSSVLYTAVQPNEGDND 1020
| | | | |
QY 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEQLELQV 1080
| | | | |
Db 1021 YIIPLPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEQLELQV 1080
| | | | |
QY 1081 EPEPELQPLDGGCPAPRAEADSFL 1106
| | | | |
Db 1081 EPEPELQPLDGGCPAPRAEADSFL 1106
| | | | |

RESULT 12
US-08-475-458-2
; Sequence 2, Application US/08475458
; Patent No. 5843725
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,458
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-475-458-2
Query Match 99.9%; Score 5762; DB 2; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVVTTPPGPELVLVNVSSTFVLTCSGSAPV 60
| | | | |
Db 1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVVTTPPGPELVLVNVSSTFVLTCSGSAPV 60
| | | | |
QY 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
| | | | |
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
| | | | |
QY 121 PDPTVGFLPNDABELFIFLTEITEITPCRVTDLPQLVVTLHEKGDVALPVYPDHQRGFS 180
| | | | |
Db 121 PDPTVGFLPNDABELFIFLTEITEITPCRVTDLPQLVVTLHEKGDVALPVYPDHQRGFS 180
| | | | |
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
| | | | |
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
| | | | |
QY 241 DVVNFETYPRKESGR LVEPVTDFLLDMPYHIRSILHIPS AELEDSGTTCNVTESVNDH 300
| | | | |
Db 241 EVVNFETYPRKESGR LVEPVTDFLLDMPYHIRSILHIPS AELEDSGTTCNVTESVNDH 300
| | | | |
QY 301 QDEKAINITVVESGYVRL LGEVGTLOFAELHRSRTLQVVF EAYPPPTVLMFKDNRTLGD S 360
| | | | |
Db 301 QDEKAINITVVESGYVRL LGEVGTLOFAELHRSRTLQVVF EAYPPPTVLMFKDNRTLGD S 360
| | | | |
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAF HEDAEVQLSFQLQINVPVRVL 420
| | | | |
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAF HEDAEVQLSFQLQINVPVRVL 420
| | | | |
QY 421 ELSSEHPDSGEQTVRCRGRMPQNPNIWSACRDLKRCRPRELPPTLLGNSSEESQLETNV 480
| | | | |
Db 421 ELSSEHPDSGEQTVRCRGRMPQNPNIWSACRDLKRCRPRELPPTLLGNSSEESQLETNV 480
| | | | |
QY 481 TYWEEEQEFVSTLR LQHVDRPLSVRCTLRNAVGODTQEVI VVPHSLPFFKVVVISAILA 540
| | | | |
Db 481 TYWEEEQEFVSTLR LQHVDRPLSVRCTLRNAVGODTQEVI VVPHSLPFFKVVVISAILA 540
| | | | |
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGH EYIYVDPMQLPYDSTWELPRDQL 600
| | | | |
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGH EYIYVDPMQLPYDSTWELPRDQL 600
| | | | |
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLK STARSSEKQALMSELKIMSHLGP 660
| | | | |
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLK STARSSEKQALMSELKIMSHLGP 660
| | | | |
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHT FLQHS DKRRPPSAE LYSNAL 720
| | | | |
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHT FLQHS DKRRPPSAE LYSNAL 720
| | | | |
QY 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
| | | | |
Db 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
| | | | |
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
| | | | |
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
| | | | |
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNS LYTTLSDVMSFGILLWEIFTLG 900
| | | | |
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNS LYTTLSDVMSFGILLWEIFTLG 900
| | | | |
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQ KCWEEKFEIRPPFSQLVLLER 960
| | | | |
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQ KCWEEKFEIRPPFSQLVLLER 960
| | | | |
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLR SP LDTSSVLYTAVQPNEGDND 1020
| | | | |

Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDND 1020

QY 1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Db 1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 13

US-08-980-400-2

; Sequence 2, Application US/08980400

; Patent No. 6018026

; GENERAL INFORMATION:

; APPLICANT: Sledziewski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; APPLICANT: Kindsvogel Ph.D., Wayne R.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,400

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/477,329

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 990008.446C6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; TELEFAX: 206-682-6031

; TELEX: 3723836

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1106 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-980-400-2

Query Match 99.9%; Score 5762; DB 3; Length 1106;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALALKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV 60

Db 1 MRLPGAMPALALKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV 60

QY 61 VWERMSQEPPOEMAKAQDGTFFSSVLTILNLTGLDTGEYFCTHNDSGLETDERKRLYIFV 120

Db 61 VWERMSQEPPOEMAKAQDGTFFSSVLTILNLTGLDTGEYFCTHNDSGLETDERKRLYIFV 120

QY 121 PDPTVGFLPNDABELFIFLITEITIPCRVTDLPQVLTLLHEKKGVDVALPVYPDHQGF 180

Db 121 PDPTVGFLPNDABELFIFLITEITIPCRVTDLPQVLTLLHEKKGVDVALPVYPDHQGF 180

QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

QY 241 DVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300

Db 241 EVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300

QY 301 ODEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

Db 301 ODEKAINITWVESGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

QY 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420

Db 361 SAGEIALSTRNVSETRYVSELTLVRVKAEGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420

QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480

Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480

QY 481 TYWEEBQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540

Db 481 TYWEEBQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540

QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600

Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600

QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660

Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660

QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHS DKRRPPSAE LYSNAL 720

Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHS DKRRPPSAE LYSNAL 720

QY 721 PVGLPLPSHVSLTGESGGYMDMSKDESVDYVPM LDKGVKYADIESSNYMAPYDNYVP 780

Db 721 PVGLPLPSHVSLTGESGGYMDMSKDESVDYVPM LDKGVKYADIESSNYMAPYDNYVP 780

QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960

Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960

QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDND 1020

Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDND 1020

QY 1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Db 1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 14

US-09-583-459A-2

; Sequence 2, Application US/09583459A

; Patent No. 6291212

; GENERAL INFORMATION:

; APPLICANT: Sledziewski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; APPLICANT: Kindsvogel Ph.D., Wayne R.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,459A
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-583-459A-2
Query Match 99.9%; Score 5762; DB 3; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV 60
QY 61 VWERMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
Db 61 VWERMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
QY 121 PDPTVGFPLNDABELFIFLTEITEITPCRVTDPPQLVVTLHEKKGVDVALPVPYDHQGF 180
Db 121 PDPTVGFPLNDABELFIFLTEITEITPCRVTDPPQLVVTLHEKKGVDVALPVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVANFEWTPRKESGRLEVPVTDFFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSNVDH 300
Db 241 EVNFEWTPRKESGRLEVPVTDFFLLDMPYHRSILHIPSAAELEDSTYTCNVTVSNVDH 300
QY 301 QDEKAINITVVEGCVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITVVEGCVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRYVSELTTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420

QY 421 ELSSEHSDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTTLGNSSEESQLETNV 480
Db 421 ELSSEHSDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTTLGNSSEESQLETNV 480
QY 481 TYWEEEOEFVSTLRLOHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEOEFVSTLRLOHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHHEYIYVDMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHHEYIYVDMQLPYDSTWELPRDQL 600
QY 601 VLGRITLCSGAFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLCSGAFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Db 661 HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQVLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQVLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSVLYTAVQPNEGDND 1020
QY 1021 YIIPDPKPVEADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPDPKPVEADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
QY 1081 EPEPELQPLDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELQPLDSGCPAPRAEAEDSFL 1106

RESULT 15
US-09-583-210-2
; Sequence 2, Application US/09583210
; Patent No. 6291646
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-583-210-2

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Query Match      99.9%; Score 5762; DB 3; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRLPGAMPALAKGELLSSLLLLLEPQISQGLVVTTPPGPELVNVSSSTFVLTCSGSAPV 60
Db      1 MRLPGAMPALAKGELLSSLLLLLEPQISQGLVVTTPPGPELVNVSSSTFVLTCSGSAPV 60

QY      61 VWERMSQEPPOEAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120
Db      61 VWERMSQEPPOEAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDNRGLTDERKRLYIFV 120

QY      121 PDPTVGFLPNDAELFIFLTTEITIPCRVTDPPQLVVTLHEKKGDVALPVYPYDHQGF 180
Db      121 PDPTVGFLPNDAELFIFLTTEITIPCRVTDPPQLVVTLHEKKGDVALPVYPYDHQGF 180

QY      181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQENITLMCIVIGN 240
Db      181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQENITLMCIVIGN 240

QY      241 DVNFEWTPYRKESGRVPEVPTDFLLDMPYHRSILHIPSAELEDSTYTCNVTVSN 300
Db      241 EVNFEWTPYRKESGRVPEVPTDFLLDMPYHRSILHIPSAELEDSTYTCNVTVSN 300

QY      301 QDEKAINITVVEGVRLLGEVGTLOFAELHRSRTLQVVEAYPPPTVLWFKDNRTL 360
Db      301 QDEKAINITVVEGVRLLGEVGTLOFAELHRSRTLQVVEAYPPPTVLWFKDNRTL 360

QY      361 SAGEIALSTRNVSETRYVSELTLRVRKVAEAGHYTMRAFHEDAEOVLSFQLQINVP 420
Db      361 SAGEIALSTRNVSETRYVSELTLRVRKVAEAGHYTMRAFHEDAEOVLSFQLQINVP 420

QY      421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQ 480
Db      421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQ 480

QY      481 TYWEEEOEFVSTLRQLQHVDRPLSVRCITLNAVQDQTOEIVVPHSLPFKVVISA 540
Db      481 TYWEEEOEFVSTLRQLQHVDRPLSVRCITLNAVQDQTOEIVVPHSLPFKVVISA 540

QY      541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWEL 600
Db      541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWEL 600

QY      601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIM 660

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Search completed: March 11, 2005, 07:50:32
Job time : 37.2478 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 04:13:19 ; Search time 129.495 Seconds
(without alignments)
3303.265 Million cell updates/sec

Title: US-10-027-400-4
Perfect score: 5766
Sequence: 1 MRLPGAMPALALKGELLLS.....EQLPDGCPAPRAEADSFL 1106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1 AAP90127	Aap90127 Platelet
2	5762	99.9	1106	2 AAR99690	Aar99690 Platelet-
3	5762	99.9	1106	6 ABP96311	Abp96311 Human pla
4	5762	99.9	1106	7 ABR84719	AbR84719 Human PDG
5	5762	99.9	1106	7 ADF45082	Adf45082 Human kin
6	5762	99.9	1106	8 ABO84679	Abo84679 Human can
7	5760	99.9	1106	6 ABG72459	Abg72459 Human pla
8	5759	99.9	1106	2 AAR26205	Aar26205 Type B hu
9	5758	99.9	1106	6 ABG72456	Abg72456 Human pla
10	5757	99.8	1106	6 ABG72458	Abg72458 Human pla
11	5756	99.8	1106	6 ABG72457	Abg72457 Human pla
12	5745.5	99.6	1107	8 ABO84677	Abo84677 Human can
13	5691	98.7	1106	1 AAP90646	Aap90646 Human pla
14	5676	98.4	1090	6 ABG72455	Abg72455 Human pla
15	5657.5	98.1	1089	4 ABG20753	Abg20753 Novel hum
16	4975	86.3	1098	8 ABO84676	Abo84676 Mouse can
17	4972	86.2	1098	5 ABB57338	Abb57338 Mouse isc
18	4857.5	84.2	1158	8 ABO84675	Abo84675 Mouse can
19	4626	80.2	2129	4 ABG15478	Abg15478 Novel hum
20	4626	80.2	2129	4 ABG20749	Abg20749 Novel hum
21	2882	50.0	561	6 ABG72460	Abg72460 Human pla
22	2796.5	48.5	821	2 AAY28935	Aay28935 Platelet-
23	2352.5	40.8	1089	6 ABG72453	Abg72453 Human pla
24	2351.5	40.8	1089	5 AAU84300	Aau84300 Human end
25	2351.5	40.8	1089	6 ABG72449	Abg72449 Human pla

26	2351.5	40.8	1089	6 ABP96312	Abp96312 Human pla
27	2351.5	40.8	1089	7 ABR84718	AbR84718 Human PDG
28	2351.5	40.8	1089	7 ADF45081	Adf45081 Human kin
29	2351.5	40.8	1089	7 ADF90896	Adf90896 Human hep
30	2351.5	40.8	1089	8 ADM69012	Adm69012 Human pla
31	2351.5	40.8	1089	8 ADQ17833	Adq17833 Human sof
32	2351.5	40.8	1089	8 ADQ59532	Adq59532 Human can
33	2351.5	40.8	1089	8 ADQ39641	Adq39641 Human myo
34	2350	40.8	1088	5 AAO17356	Aao17356 Human pla
35	2349.5	40.7	1089	2 AAR06910	Aar06910 Alpha typ
36	2348.5	40.7	1089	2 AAR08267	Aar08267 Platelet
37	2347.5	40.7	1089	6 ABG72450	Abg72450 Human pla
38	2346.5	40.7	1089	6 ABG72452	Abg72452 Human pla
39	2345.5	40.7	1089	6 ABG72451	Abg72451 Human pla
40	2344.5	40.7	1089	8 ADM69031	Adm69031 Human PDG
41	2342.5	40.6	1089	8 ADM69014	Adm69014 Human PDG
42	2339.5	40.6	1089	8 ADM69035	Adm69035 Human PDG
43	2336.5	40.5	1090	8 ADM69020	Adm69020 Human PDG
44	2324.5	40.3	1085	8 ADM69016	Adm69016 Human PDG
45	2322	40.3	1086	8 ADM69018	Adm69018 Human PDG

ALIGNMENTS

RESULT 1
AAP90127
ID AAP90127 standard; protein; 1106 AA.

XX AAP90127;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Platelet derived growth factor receptor.
XX
KW Platelet derived growth factor receptor; human;
KW ligand binding receptor analogues; isoforms; assays; antibodies;
KW atherosclerosis; wound healing; peptide dimer; cDNA.
OS Homo sapiens.
XX
PN EP325224-A.
XX
PD 26-JUL-1989.
XX
PF 18-JAN-1989; 89EP-00100787.
XX
PR 22-JAN-1988; 88US-00146877.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Siedziewsk AZ, Bell LA, Kindsvogel WR;
XX
DR WPI; 1989-214434/30.
DR N-PSDB; AAN90355.
XX
PT Secreted ligand-binding receptor analogues e.g. PDGF receptor - used in assays, in purifications and as or with therapeutic agents.
XX
PS Claim 2; Fig 1; 45pp; English.
XX
CC Platelet derived growth factor receptor (see corresp. AAN90355). Used in the invention to make analogues that are secreted (pref. Ile-29 - Met-441, and Ile-29 - Lys-531; see specification for details). These analogues are easily purified, produced in large quantities recombinantly, used to produce antibodies, to screen ligands as imaging agents, as (ant-)agonists, or therapeutically for atherosclerosis and wound healing, and assays. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 1; Length 1106;

Best Local Similarity 99.9%; Pred. No. 0;		Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MRLPGAMPALALKGELLILLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV	60
Db	1	MRLPGAMPALALKGELLILLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV	60
Qy	61	VVERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDSRGLTDERKRLYIFV	120
Db	61	VVERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDSRGLTDERKRLYIFV	120
Qy	121	PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQGF	180
Db	121	PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQGF	180
Qy	181	GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Db	181	GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Qy	241	DVYNFEWTPRKESGRLEVPVTDFLDMPYHIRSILHIPSAALEDSGTYTCNVTESVNDH	300
Db	241	EVVNFEWTPRKESGRLEVPVTDFLDMPYHIRSILHIPSAALEDSGTYTCNVTESVNDH	300
Qy	301	QDEKAINITVVESGYVRLLEGEVGTLOFAELHRSRTLQVVFAYPPPTVLWFKDNRILGDS	360
Db	301	QDEKAINITVVESGYVRLLEGEVGTLOFAELHRSRTLQVVFAYPPPTVLWFKDNRILGDS	360
Qy	361	SAGEIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL	420
Db	361	SAGEIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL	420
Qy	421	ELSESHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Db	421	ELSESHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Qy	481	TYWEEQEFVWSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFKVVISAILA	540
Db	481	TYWEEQEFVWSTLRLQHVDRPLSVRCTLRNAVQDQTOEVIIVPHSLPFKVVISAILA	540
Qy	541	LVVLTIIISLIILIMLWQKKPRYRIRWKVIESVSSDGHEIYVDPMQLPYDSTWELPRDQL	600
Db	541	LVVLTIIISLIILIMLWQKKPRYRIRWKVIESVSSDGHEIYVDPMQLPYDSTWELPRDQL	600
Qy	601	VLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	660
Db	601	VLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	660
Qy	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAEYSNAL	720
Db	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAEYSNAL	720
Qy	721	PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP	780
Db	721	PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP	780
Qy	781	SAPERTCRATLINESPVLSDVLGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLV	840
Db	781	SAPERTCRATLINESPVLSDVLGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLV	840
Qy	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	900
Db	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	900
Qy	901	GTPPELPMNEQFYNAIKRGYRNAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER	960
Db	901	GTPPELPMNEQFYNAIKRGYRNAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER	960
Qy	961	LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLDTSSSVLYTAVQPNEGDND	1020
Db	961	LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLDTSSSVLYTAVQPNEGDND	1020
Qy	1021	YIILPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080

Db	1021	YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV	1080
QY	1081	EPEPELEQLPDSGCPAPRAEADSFL	1106
Db	1081	EPEPELEQLPDSGCPAPRAEADSFL	1106
RESULT 2			
AAR99690			
ID	AAR99690 standard; protein; 1106 AA.		
XX	AAR99690;		
XX	AC		
DT	25-MAR-2003 (revised)		
DT	11-OCT-1996 (first entry)		
XX	Platelet-derived growth factor receptor.		
XX	Platelet-derived growth factor receptor; PDGF-R; peptide dimer;		
KW	protein secretion; agonist; antagonist.		
XX	Homo sapiens.		
OS	EP721983-A1.		
XX	17-JUL-1996.		
XX	18-JAN-1989; 95EP-00118567.		
XX	22-JAN-1988; 88US-00146877.		
PR	18-JAN-1989; 89EP-00100787.		
XX	(ZYMO) ZYMOGENETICS INC.		
PI	Sledziewski AZ, Bell LA, Kindsvogel WR;		
XX	WPI; 1996-322833/33.		
DR	N-PSDB; AAT34552.		
XX	Prodn. of biologically active peptide dimers, esp. platelet-derived growth factor receptor analogues - useful for systematic designing of novel (ant)agonists.		
PS	Disclosure; Fig 1; 45pp; English.		
XX	The amino acid sequence (AAR99690) of human platelet-derived growth factor receptor (PDGF-R) was deduced from a cDNA clone (AAT34552) isolated from a human diploid dermal fibroblast library. The cDNA can be used in novel constructs that allow the prodn. of secreted biologically active PDGF-R analogues. This may comprise linking a sequence coding for PDGR-R, or the ligand- binding domain of the PDGF-R extracellular region, to a protein secretion signal (e.g. SUC2) and promoter, and expressed in transformed host cells, esp. Saccharomyces cerevisiae. The secreted PDGF-R analogues are used in ligand screening procedures, to screen for (ant)agonists, and in diagnostic assays. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)		
SQ	Sequence 1106 AA;		
Query Match 99.9%; Score 5762; DB 2; Length 1106;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MRLPGAMPALALKGELLILLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV	60
Db	1	MRLPGAMPALALKGELLILLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV	60
QY	61	VVERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDSRGLTDERKRLYIFV	120
Db	61	VVERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNDSRGLTDERKRLYIFV	120
QY	121	PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQGF	180

Db 121 PDPTVGFLPNDAAELFIFLTFEITETIPCRVTDPLQVLTLHEKKGDVLPVPYDHQGRFS 180

Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Qy 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELEDSTGTYTCNVTESVNDH 300

Db 241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELEDSTGTYTCNVTESVNDH 300

Qy 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

Db 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420

Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420

Qy 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480

Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480

Qy 481 TYWEEBQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540

Db 481 TYWEEBQEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540

Qy 541 LVVLTIIISLIILIMLWQKPKRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600

Db 541 LVVLTIIISLIILIMLWQKPKRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600

Qy 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSLKIMSHLGP 660

Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSLKIMSHLGP 660

Qy 661 HLNVNLLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLOHSHDKRRPPSAELYSNAL 720

Db 661 HLNVNLLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLOHSHDKRRPPSAELYSNAL 720

Qy 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADI ESSNYMAPYDNYVP 780

Db 721 PVGLPLPSHVS LTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADI ESSNYMAPYDNYVP 780

Qy 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDWVSFGILLWEIFTLG 900

Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDWVSFGILLWEIFTLG 900

Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960

Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960

Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020

Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020

Qy 1021 YTIPLDPKPKEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Db 1021 YTIPLDPKPKEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Qy 1081 EPEPELQLPDSCGCPAPRAEADSFL 1106

Db 1081 EPEPELQLPDSCGCPAPRAEADSFL 1106

RESULT 3
ABP96311
ID ABP96311 standard; protein; 1106 AA.
XX
AC ABP96311;
XX

DT 20-MAY-2003 (first entry)

XX Human platelet-derived growth factor receptor beta protein.

XX

KW Humanised baculovirus; cytostatic; gene therapy; baculovirus; cancer;
KW prostate cancer; platelet-derived growth factor receptor beta;
KW chromosome 5.

XX Homo sapiens.

OS

XX WO2003016540-A2.

PN

XX 27-FEB-2003.

PD

XX 15-AUG-2002; 2002WO-GB003791.

PF

XX 15-AUG-2001; 2001GB-00019852.

PR

XX (UYYO-) UNIV YORK.

PA

XX Maitland N;

PI

XX WPI; 2003-268336/26.

DR

XX New baculovirus having a modified genome encoding a therapeutic agent,
PT useful in the manufacture of a medicament for the treatment of cancer,
PT particularly prostate cancer.

XX

PS Claim 33; Page; 34pp; English.

XX

CC The present invention describes a humanised baculovirus (I) which
CC comprises a modified baculovirus genome having a nucleic acid molecule
CC encoding a therapeutic agent and a polypeptide which functions to target
CC the baculovirus to at least one cell type. Also described is a
CC pharmaceutical composition comprising (I). (I) has cytostatic activity,
CC and can be used in gene therapy. The baculovirus is useful in the
CC manufacture of a medicament for the treatment of cancer, particularly
CC prostate cancer. The present sequence represents the human platelet-
CC derived growth factor receptor beta protein, which is specified in the
CC exemplification of the present invention. N.B. The present sequence is
CC not given in the specification but is referred to in Claim 33 as Genbank
CC accession number NM_002609

XX

SQ Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 6; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLPGAMPALALKGELLSSLLLEPQISQGLVVTTPPGBELVNVSSFTVLTCSGSAV 60

Db 1 MRLPGAMPALALKGELLSSLLLEPQISQGLVVTTPPGBELVNVSSFTVLTCSGSAV 60

Qy 61 VWERMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120

Db 61 VWERMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120

Qy 121 PDPTVGFLPNDAAELFIFLTFEITETIPCRVTDPLQVLTLHEKKGDVLPVPYDHQGRFS 180

Db 121 PDPTVGFLPNDAAELFIFLTFEITETIPCRVTDPLQVLTLHEKKGDVLPVPYDHQGRFS 180

Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Qy 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELEDSTGTYTCNVTESVNDH 300

Db 241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELEDSTGTYTCNVTESVNDH 300

Qy 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

Db 301 QDEKAINITVVEGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360

QY	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDA	AEVQLSFQLQINVPVRVL	420
Db	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDA	AEVQLSFQLQINVPVRVL	420
QY	421	ELSESHPSGEOQVRCRGRMPQPNIIWSACRDLKRCPRELPTTL	LGNSSEESQLETNV	480
Db	421	ELSESHPSGEOQVRCRGRMPQPNIIWSACRDLKRCPRELPTTL	LGNSSEESQLETNV	480
QY	481	TYWEEEOQEFVSVTLRLQHVDRPLSVRCTLRNAVGDQTQEVIV	PHSLPFKVVISAILA	540
Db	481	TYWEEEOQEFVSVTLRLQHVDRPLSVRCTLRNAVGDQTQEVIV	PHSLPFKVVISAILA	540
QY	541	LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHEYIYV	DPMLPYDSTWELPRDQL	600
Db	541	LVVLTIIISLIILMLWQKKPRYEIRWKVIESVSSDGHEYIYV	DPMLPYDSTWELPRDQL	600
QY	601	VLGRTLGSAGFGVVEATAHGLSHSQATMKVAVKMLKSTAR	SEKQALMSELKIMSHLGP	660
Db	601	VLGRTLGSAGFGVVEATAHGLSHSQATMKVAVKMLKSTAR	SEKQALMSELKIMSHLGP	660
QY	661	HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFL	QHHSCKRRRPPSAEYLSNAL	720
Db	661	HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFL	QHHSCKRRRPPSAEYLSNAL	720
QY	721	PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMG	DKVYADIESSNYMAPYDNYVP	780
Db	721	PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMG	DKVYADIESSNYMAPYDNYVP	780
QY	781	SAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNC	VHRDLAARNVLICEGKLV	840
Db	781	SAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNC	VHRDLAARNVLICEGKLV	840
QY	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLY	TTLSDVWSFGILLWEIFTLG	900
Db	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLY	TTLSDVWSFGILLWEIFTLG	900
QY	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQK	WEEKFEIRPPFSQLVLLER	960
Db	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQK	WEEKFEIRPPFSQLVLLER	960
QY	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLR	SPLDTSSVLYTAVQNEGNDND	1020
Db	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLR	SPLDTSSVLYTAVQNEGNDND	1020
QY	1021	YIIPLPDPKPEVADEGPLEGSPSLASSTLTNEVNTSSTIS	CDSPLEPQDEPEPEQLELOV	1080
Db	1021	YIIPLPDPKPEVADEGPLEGSPSLASSTLTNEVNTSSTIS	CDSPLEPQDEPEPEQLELOV	1080
QY	1081	EPEPELEQLPDSGCAPRAEAEДСFL	1106	
Db	1081	EPEPELEQLPDSGCAPRAEAEДСFL	1106	

RESULT 4	
ABR84719	
ID	ABR84719 standard; protein; 1106 AA.
XX	
AC	ABR84719;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human PDGF beta receptor protein.
XX	
KW	Tissue vascularisation; aging; mouse; human; PDGF A; PDGF B;
KW	PDGF alpha receptor; PDGF beta receptor; endothelial precursor cell;
KW	vascular disease; cardiant; celltherapy.

13-FEB-2003; 2003WO-US004244 .

15-FEB-2002; 2002US-0357328P .

08-AUG-2002; 2002WO-US025175 .

(CORR) CORNELL RES FOUND INC .

(EDEL/) EDELBERG J M .

(RAFI/) RAFII S .

(HONG/) HONG M K .

(LANZ/) LANZA R P .

(WEST/) WEST M D .

Edelberg JM, Rafii S, Hong MK, Lanza RP, West MD;

WPI; 2003-697548/66 .

Treating a vascular condition, e.g. myocardial infarction, atherosclerosis, ischemia, congestive heart failure, hypertension, stroke, thrombosis, arrhythmia or tachycardia, by administering endothelial precursor cells .

Claim 24; Page 47-48; 110pp; English .

The present invention relates to a method of treating a vascular condition in a mammal, which comprises administering to the mammal a therapeutic amount of endothelial precursor cells . The method and cells of the invention are useful for treating a vascular condition, e.g. myocardial infarction, atherosclerosis, ischaemia, tachycardia, congestive heart failure, peripheral vasculature disorder, hypertension, stroke, thrombosis, arrhythmia or tachycardia . The present sequence is a protein shown in the exemplification of the invention

Sequence 1106 AA;

	Query Match	99.9%;	Score 5762;	DB 7;	Length11106;																																																		
	Best Local Similarity	99.9%;	Pred. No. 0;																																																				
	Matches 1105;	Conservative	1;	Mismatches 0;	Indels 0; Gaps 0;																																																		
Qy	1	MRLPGAMPALAKGELL	LLSLL	LLLEPQISQGLVVT	PPGPELVLVNSSTFVLTCSGSA	PV 60																																																	
Db	1	MRLPGAMPALAKGELL	LLSLL	LLLEPQISQGLVVT	PPGPELVLVNSSTFVLTCSGSA	PV 60																																																	
Qy	61	VWERM	SQEP	PQEMAKAQD	GFSSVLT	LTNL	TGLD	TGEY	FCTH	ND	SR	GLET	DER	KRL	YIF	V 120																																							
Db	61	VWERM	SQEP	PQEMAKAQD	GFSSVLT	LTNL	TGLD	TGEY	FCTH	ND	SR	GLET	DER	KRL	YIF	V 120																																							
Qy	121	PDPT	VGFL	PND	AEL	FIFL	TEIT	EIT	PCR	VT	DP	Q	L	V	V	T	L	HEK	K	G	D	V	A	L	P	V	P	Y	D	H	Q	R	G	F	S 180																				
Db	121	PDPT	VGFL	PND	AEL	FIFL	TEIT	EIT	PCR	VT	DP	Q	L	V	V	T	L	HEK	K	G	D	V	A	L	P	V	P	Y	D	H	Q	R	G	F	S 180																				
Qy	181	GIFED	RSYI	CK	TTI	G	D	R	E	V	D	S	D	A	Y	Y	V	R	L	Q	V	S	S	I	N	V	S	N	A	V	Q	T	V	R	Q	E	N	I	T	L	M	C	I	V	I	G	N 240								
Db	181	GIFED	RSYI	CK	TTI	G	D	R	E	V	D	S	D	A	Y	Y	V	R	L	Q	V	S	S	I	N	V	S	N	A	V	Q	T	V	R	Q	E	N	I	T	L	M	C	I	V	I	G	N 240								
Qy	241	DVNF	EW	TY	PR	K	E	S	R	L	V	E	P	V	T	D	F	L	L	D	M	P	Y	H	I	R	S	I	L	H	I	P	S	A	E	L	D	S	G	T	Y	T	C	N	V	T	E	S	V	N	D	H 300			
Db	241	EVNF	EW	TY	PR	K	E	S	R	L	V	E	P	V	T	D	F	L	L	D	M	P	Y	H	I	R	S	I	L	H	I	P	S	A	E	L	D	S	G	T	Y	T	C	N	V	T	E	S	V	N	D	H 300			
Qy	301	QDEK	A	I	N	I	T	V	V	E	S	G	V	R	L	L	G	E	V	G	T	L	Q	F	A	E	L	H	R	S	R	T	L	Q	V	F	E	A	Y	P	P	T	V	L	W	F	K	D	N	R	T	L	G	D	S 360
Db	301	QDEK	A	I	N	I	T	V	V	E	S	G	V	R	L	L	G	E	V	G	T	L	Q	F	A	E	L	H	R	S	R	T	L	Q	V	F	E	A	Y	P	P	T	V	L	W	F	K	D	N	R	T	L	G	D	S 360
Qy	361	SAGE	I	A	L	S	T	R	N	V	S	E	T	R	Y	V	S	E	L	T	L	V	R	K	V	A	E	A	G	H	Y	T	M	R	A	F	H	E	D	A	E	V	Q	L	S	F	Q	L	I	N	V	P	R	V	L 420
Db	361	SAGE	I	A	L	S	T	R	N	V	S	E	T	R	Y	V	S	E	L	T	L	V	R	K	V	A	E	A	G	H	Y	T	M	R	A	F	H	E	D	A	E	V	Q	L	S	F	Q	L	I	N	V	P	R	V	L 420
Qy	421	ELSE	S	H	P	D	S	G	E	Q	T	V	R	C	R	G	R	G	M	P	Q	N	I	I	W	S	A	C	R	D	L	K	C	P	R	E	L	P	P	T	L	L	G	N	S	S	E	E	S	Q	L	E	T	N	V 480
Db	421	ELSE	S	H	P	D	S	G	E	Q	T	V	R	C	R	G	R	G	M	P	Q	N	I	I	W	S	A	C	R	D	L	K	C	P	R	E	L	P	P	T	L	L	G	N	S	S	E	E	S	Q	L	E	T	N	V 480
Qy	481	TYWEE	E	E	E	E	E	F	E	V	V	S	T	L	R	L	Q	H	V	D	R	P	L	S	V	R	C	T	L	R																									

Qy 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDWVSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDWVSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSLDTSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSLDTSVLYTAVQPNEGDND 1020
Qy 1021 YIIPDPKPVEADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPDPKPVEADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Qy 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

RESULT 5

ADF45082
ID ADF45082 standard; protein; 1106 AA.

XX ADF45082;

DT 12-FEB-2004 (first entry)

XX Human kinase PDGFR-b.

KW Human; protein kinase; enzyme; inhibitor; PDGFR-b.

XX Homo sapiens.

PN WO2003081210-A2.

PD 02-OCT-2003.

PF 20-MAR-2003; 2003WO-US0008725.

PR 21-MAR-2002; 2002US-0366892P.

XX (SUNE-) SUNESIS PHARM INC.

XX Prescott JC, Braisted A;

XX WPI; 2003-865136/80.

XX Identifying ligand binding to inactive conformation of target protein
PT kinase (r) comprises contacting the conformation modified (r) which
PT contains reactive group at binding site, with ligands and detecting

PT kinase-ligand conjugate formation.

XX Disclosure; SEQ ID NO 51; 260pp; English.

XX The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.

XX Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 7; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPLGAMPALALKGELLILLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV 60
Db 1 MRPLGAMPALALKGELLILLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSGSAPV 60
Qy 61 VVERMSQEPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHNSRGLETDERKRLYIFV 120
Db 61 VVERMSQEPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHNSRGLETDERKRLYIFV 120
Qy 121 PDPVTGFLPNDAAELFIFLITEITEITIPCRVTDLPQLVVTLHEKKGDVALPVPYDHQRGFS 180
Db 121 PDPVTGFLPNDAAELFIFLITEITEITIPCRVTDLPQLVVTLHEKKGDVALPVPYDHQRGFS 180
Qy 181 GIFEDRSYICKTTIGDREVSDAYYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Qy 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
Db 241 EVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
Qy 301 QDEKAINITWESGYVRLIGEVGTLOFAELHRSRTLQVVEAYPPPTLVWFKDNRTLGD 360
Db 301 QDEKAINITWESGYVRLIGEVGTLOFAELHRSRTLQVVEAYPPPTLVWFKDNRTLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
Qy 421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCRELPPPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCRELPPPTLLGNSSEESQLETNV 480
Qy 481 TYWEEEEEQEFVSTLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEEEQEFVSTLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPHSLPFKVVVISAILA 540
Qy 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780

Qy 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLER 960
Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYTAVQPNEGDND 1020
Qy 1021 YIIPLDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Qy 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106

RESULT 6
ABO84679
ID ABO84679 standard; protein; 1106 AA.
XX ABO84679;
AC ABO84679;
XX ABO84679;
DT 18-NOV-2004 (first entry)
XX Human cancer-associated protein HP20-018.3.
DE Human cancer-associated protein; cytostatic; cancer; leukaemia;
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX Homo sapiens.
OS WO2004074320-A2.
PN 02-SEP-2004.
XX 17-FEB-2004; 2004WO-US004730.
XX 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-0038838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
PA Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
DR N-PSDB; ABD32965.

XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX claim 18; segid 710; 310pp; English.
PS The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe

CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells(comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 8; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLPGAMPALALKGELLSSLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV 60
Db 1 MRLPGAMPALALKGELLSSLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV 60
Qy 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGDTGEYFCTHNDSRGLETDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGDTGEYFCTHNDSRGLETDERKRLYIFV 120
Qy 121 PDPTVGFLPNDAAELFIFLITEITEITPCRVTDPQLVVTLHEKKGDVALPVPYDHQGF 180
Db 121 PDPTVGFLPNDAAELFIFLITEITEITPCRVTDPQLVVTLHEKKGDVALPVPYDHQGF 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQENITLMCIVGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQENITLMCIVGN 240
Qy 241 DVVNFETWYPRKESGRVVEPTDFLLDMPYHIRSILHIPSAAELEDSTYTCNVTESVNDH 300
Db 241 EVVNFETWYPRKESGRVVEPTDFLLDMPYHIRSILHIPSAAELEDSTYTCNVTESVNDH 300
Qy 301 QDEKAINITVVESGYVRLGEGVGTLOFAELHRSRTLQVVEAYPPPTVLWFKDNRITLGD 360
Db 301 QDEKAINITVVESGYVRLGEGVGTLOFAELHRSRTLQVVEAYPPPTVLWFKDNRITLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420
Qy 421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCRELPTTLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLKRCRELPTTLGNSSEESQLETNV 480
Qy 481 TYWEEEQEFVWSTLRLQHVDRPLSVRCCTLRNAVGDQTEQVIWPHSLPFFKVVISAILA 540
Db 481 TYWEEEQEFVWSTLRLQHVDRPLSVRCCTLRNAVGDQTEQVIWPHSLPFFKVVISAILA 540
Qy 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHGYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHGYIYVDPMQLPYDSTWELPRDQL 600
Qy 601 VLGRTLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660

Db 601 VLGRTLGSGAFQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660

Qy 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHFTLQHSDKRRPPSAELYSNAL 720

Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHFTLQHSDKRRPPSAELYSNAL 720

Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADIESSNYMAPYDNYVP 780

Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPM LDMKGDVKYADIESSNYMAPYDNYVP 780

Qy 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960

Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960

Qy 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020

Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020

Qy 1021 YIIPLPDPKPEVADEGPLEGSSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Db 1021 YIIPLPDPKPEVADEGPLEGSSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Qy 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

RESULT 7

ABG72459

ID ABG72459 standard; protein; 1106 AA.

XX

AC ABG72459;

XX

DT 13-FEB-2003 (first entry)

XX

DE Human platelet derived growth factor receptor beta mutant L867M.

XX

KW Human; platelet derived growth factor receptor beta; PDGFRbeta;

KW hepatotropic; dermatological; nephrotropic; vulnerable; ophthalmological;

KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;

KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;

KW cell migration; extracellular matrix synthesis; secretion;

KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;

KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;

KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;

KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .32

FT /label= Signal_peptide

FT Protein 33. .1106

FT /label= Mature_PDGR_beta

FT Domain 227. .298

FT /label= Immunoglobulin-like_domain

FT Domain 335. .398

FT /label= Immunoglobulin-like_domain

FT Domain 532. .556

FT /label= Transmembrane_domain

FT Domain 604. .694

FT /note= "Split tyrosine kinase domain segment 1"

FT Domain 799. .951

FT /note= "Split tyrosine kinase domain segment 2"

FT Misc-difference 867

FT /note= "Wild type Leu substituted by Met"

XX

PN US2002111304-A1.

XX

PD 15-AUG-2002.

XX

PD 25-MAY-2001; 2001US-00866510.

PF

XX

PR 01-DEC-2000; 2000US-0250747P.

PR 07-MAY-2001; 2001US-0289103P.

XX

PA (KAZL/) KAZLAUSKAS A.

PA (IKUN/) IKUNO Y.

XX

PI Kazlauskas A, Ikuno Y;

XX

DR WPI; 2003-066697/06.

DR N-PSDB; ABS57790.

XX

PT New polypeptide for treating or preventing diseases associated with an

PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell

PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha

PT or -beta.

XX

PS Claim 7; Page 101-104; 127pp; English.

XX

CC The invention describes a polypeptide comprising a portion of the

CC receptor tyrosine kinase platelet-derived growth factor alpha receptor

CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in

CC treating or preventing diseases and conditions associated with an

CC abnormal PDGF level or response, such as cell proliferation, cell

CC migration, extracellular matrix synthesis and secretion or cell

CC contraction. Exemplary diseases or disorders include cell proliferative

CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.

CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,

CC scleroderma, keloids, hypertrophic scars, skin wound healing or

CC proliferative vitreoretinopathy). The method may be used in identifying

CC compounds for treating or preventing the development of diseases

CC involving cell contraction, e.g. fibrotic diseases. This is the amino

CC acid sequence of human platelet derived growth factor receptor (PDGFR)

CC beta mutant L867M

XX

SQ Sequence 1106 AA;

Query Match 99.9%; Score 5760; DB 6; Length 1106;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLPGAMPALALKGELLLSLLLEPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60

Db 1 MRLPGAMPALALKGELLLSLLLEPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60

Qy 61 VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120

Db 61 VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120

Qy 121 PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVLPVPYDHQGF 180

Db 121 PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVLPVPYDHQGF 180

Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVGN 240

Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVGN 240

Qy 241 DVVNFETYPRKESGRVPEVPTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300

Db 241 EVVNFETYPRKESGRVPEVPTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300

Qy 301 QDEKAINITVVESGYVRLGGEVGTLOFAELHRSRTLQVVF EAYPPPTVLWFKDNRTLGD 360

Db 301 QDEKAINITVVESGYVRLGGEVGTLOFAELHRSRTLQVVF EAYPPPTVLWFKDNRTLGD 360

QY 361 SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420
Db SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPELPTLLGNSSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPELPTLLGNSSSEESQLETNV 480
QY 481 TYWEEEQEFVWSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEQEFVWSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEIYVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRTLGSGAFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
Db 601 VLGRTLGSGAFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
QY 661 HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHITFLOHSHDKRRPPSAELYSNAL 720
Db 661 HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHITFLOHSHDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGVNDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGVNDMSKDESVDYVPMMDKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
Db 1021 YIIPLPDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
RESULT 8
ID AAR26205 standard; protein; 1106 AA.
XX
AC AAR26205;
XX
DT 25-MAR-2003 (revised)
DT 09-FEB-1993 (first entry)
XX
DE Type B human platelet-derived growth factor receptor.
XX
KW PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..32
FT /label= Signal_peptide
FT Protein 24..1106

/label= Mature_PDGF-B
WO9213867-A1.
20-AUG-1992.
28-JAN-1992; 92WO-US000730.
31-JAN-1991; 91US-00650793.
(CORT-) COR THERAPEUTICS INC.
Escobedo JA, Williams LT, Wolf D, Tomlinson JE, Fretto LJ, Giese NA;
WPI; 1992-299970/36.
N-PSDB; AAQ27447.
Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful as therapeutic and diagnostic agents e.g. for assaying PDGF activity in sample.
Disclosure; Page 75; 109pp; English.
The sequence given is one allele of type B human platelet-derived growth factor (PDGF) receptor (PDGF-R). This receptor is typically found on cells of mesenchymal origin. It acts while in the form of two transmembrane glycoproteins, each of which is about 180 kD. This receptor has three major regions. The first is a transmembrane region, which spans the membrane once, separating the regions of the receptor exterior to the cell from those interior to the cell. The second region is an extracellular region which contains the domains which bind the PDGF. The third region is an intracellular region which possesses a tyrosine kinase activity. This tyrosine kinase domain is notable in having an insert of approx. 100 amino acids, as compared with most other receptor tyrosine kinase domains which are contiguous or have shorter insert sequences. Fragments of this sequence between 8 and 400 amino acids comprising one or more PDGF ligand binding region from the extracellular domain may be used to bind a PDGF ligand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1106 AA;

Query Match 99.9%; Score 5759; DB 2; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLPGAMPALALKGELLSLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV 60
Db 1 MRLPGAMPALALKGELLSLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV 60
QY 61 VVERMSQEPPEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
Db 61 VVERMSQEPPEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV 120
QY 121 PDPTVGFLPNDAAELFIFLITEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQGF 180
Db 121 PDPTVGFLPNDAAELFIFLITEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIVIGN 240
QY 241 DVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
Db 241 DVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
QY 301 QDEKAINITVVEGSGYVRLGEGVGTQFAELHRSRTLQVVEAYPPPTVLWFKDNRTLGD 360
Db 301 QDEKAINITVVEGSGYVRLGEGVGTQFAELHRSRTLQVVEAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420

Db 121 PDPTVGFLPNDAAELFIFLTFEITIPCRVTDLPQLVVTLHEKKGDAVALPVPYDHQGF 180
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELSDSGTYTCNVTVSNDH 300
Db 241 EVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAAELSDSGTYTCNVTVSNDH 300
QY 301 ODEKAINITVVEGYVRLGEGVGTLPQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
Db 301 ODEKAINITVVEGYVRLGEGVGTLPQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGD 360
QY 361 SAGEIALSTNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAELVQLSFQLQINVPVRVL 420
Db 361 SAGEIALSTNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAELVQLSFQLQINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEEQBEFVSTLRLQHVDRPLSVRCTLRNAGVQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEEQBEFVSTLRLQHVDRPLSVRCTLRNAGVQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWKLPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWKLPRDQL 600
QY 601 VLGRITLGSAGFQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMDKMGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840
Db 781 SAPERTCRATLINESPVL SYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
Db 1021 YIIPLPDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080
QY 1081 EPEPELQLPDSCGPAPRAEADSFL 1106
Db 1081 EPEPELQLPDSCGPAPRAEADSFL 1106

RESULT 10

ABG72458

ID ABG72458 standard; protein; 1106 AA.

XX

AC ABG72458;

XX 13-FEB-2003 (first entry)
DT Human platelet derived growth factor receptor beta mutant D826N.
XX
DE Human; platelet derived growth factor receptor beta; PDGFRbeta;
KW hepatotropic; dermatological; nephrotropic; vulnary; ophthalmological;
KW cytosatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW mutant; mutin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..32
FT /label= Signal_peptide
FT Protein 33..1106
FT /label= Mature_PDGFR_beta
FT Domain 227..298
FT /label= Immunoglobulin-like_domain
FT Domain 335..398
FT /label= Immunoglobulin-like_domain
FT Domain 532..556
FT /label= Transmembrane_domain
FT Domain 604..694
FT /note= "Split tyrosine kinase domain segment 1"
FT 799..951
FT /note= "Split tyrosine kinase domain segment 2"
FT Misc-difference 826
FT /note= "Wild type Asp substituted by Asn"
XX
US2002111304-A1.
XX
PN 15-AUG-2002.
XX
PD 25-MAY-2001; 2001US-00866510.
XX
PF 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
XX
XX (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
PA
XX Kazlauskas A, Ikuno Y;
PI
XX WPI; 2003-066697/06.
DR N-PSDB; ABS57789.
DR
XX New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 95-97; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalpha). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino

CC	acid sequence of human platelet derived growth factor receptor (PDGFR)	
CC	beta mutant D826N	
XX		
SQ	Sequence 1106 AA;	
	Query Match 99.8%; Score 5757; DB 6; Length 1106;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60	961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPLDTSSVLVTAVQPNEGND 1020
Db	1 MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVTPPGPELVNVSSTFVLTCSGSAPV 60	961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPLDTSSVLVTAVQPNEGND 1020
Qy	61 VWERMSQEPPQEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLETDERKRLYIFV 120	1021 YIIPLPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
Db	61 VWERMSQEPPQEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLETDERKRLYIFV 120	1021 YIIPLPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
Qy	121 PDPTVGFLPNDAEELFIFLTFEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQRGFS 180	1081 EPEPELEQLPDGCGCPAPRAEAEDSFL 1106
Db	121 PDPTVGFLPNDAEELFIFLTFEITIPCRVTDPPQLVVTLHEKKGDVALPVPYDHQRGFS 180	1081 EPEPELEQLPDGCGCPAPRAEAEDSFL 1106
Qy	181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240	
Db	181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240	
Qy	241 DVNPEWPTYPRKESGRLEVPTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDH 300	
Db	241 EVNPEWPTYPRKESGRLEVPTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDH 300	
Qy	301 QDEKAINITVVESGYVRLGEGVTLQFAELHRSRTLQVVEAYPPPTVLWFKDNRTLGD 360	
Db	301 QDEKAINITVVESGYVRLGEGVTLQFAELHRSRTLQVVEAYPPPTVLWFKDNRTLGD 360	
Qy	361 SAGEIALSTRNVSETRYVSELTLVVRKVVAEAGHYTMRAFHEDAELVQLSFQLQINVPVRVL 420	
Db	361 SAGEIALSTRNVSETRYVSELTLVVRKVVAEAGHYTMRAFHEDAELVQLSFQLQINVPVRVL 420	
Qy	421 ELSESHPSDGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480	
Db	421 ELSESHPSDGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480	
Qy	481 TYWEEEQEFEVVSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540	
Db	481 TYWEEEQEFEVVSTLRQLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540	
Qy	541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHIEYIVDPMQLPYDSTWELPRDQL 600	
Db	541 LVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGHIEYIVDPMQLPYDSTWELPRDQL 600	
Qy	601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSKEQALMSSELKIMSHLGP 660	
Db	601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSKEQALMSSELKIMSHLGP 660	
Qy	661 HLNVVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720	
Db	661 HLNVVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720	
Qy	721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDKMGDVKYADIESSNYMAPYDNYVP 780	
Db	721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDKMGDVKYADIESSNYMAPYDNYVP 780	
Qy	781 SAPERTCRATLINESPVL SYMDLVGF SYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840	
Db	781 SAPERTCRATLINESPVL SYMDLVGF SYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840	
Qy	841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900	
Db	841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900	
Qy	901 GTPYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960	
Db	901 GTPYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER 960	
Qy		RESULT 11
Db		ABG72457
XX	ID ABG72457 standard; protein; 1106 AA.	
AC	ABG72457;	
XX		
DT	13-FEB-2003 (first entry)	
DE	Human platelet derived growth factor receptor beta mutant T672M.	
XX		
KW	Human; platelet derived growth factor receptor beta; PDGFRbeta;	
KW	hepatotropic; dermatological; nephrotropic; vulnery; ophthalmological;	
KW	cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;	
KW	phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;	
KW	cell migration; extracellular matrix synthesis; secretion;	
KW	cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;	
KW	liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;	
KW	keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;	
KW	mutant; mutein.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1. .32
FT		/label= Signal_peptide
FT	Protein	33. .1106
FT		/label= Mature_PDGFR_beta
FT	Domain	227. .298
FT		/label= Immunoglobulin-like_domain
FT	Domain	335. .398
FT		/label= Immunoglobulin-like_domain
FT	Domain	532. .556
FT		/label= Transmembrane_domain
FT	Domain	604. .694
FT		/note= "Split tyrosine kinase domain segment 1"
FT	Misc-difference 672	
FT		/note= "Wild type Thr substituted by Met"
FT	Domain	799. .951
FT		/note= "Split tyrosine kinase domain segment 2"
XX		US2002111304-A1.
PN		15-AUG-2002.
XX		25-MAY-2001; 2001US-00866510.
PF		01-DEC-2000; 2000US-0250747P.
XX		07-MAY-2001; 2001US-0289103P.
PR		(KAZL/) KAZLAUSKAS A.
XX		(IKUN/) IKUNO Y.
PA		Kazlauskas A, Ikuno Y;
XX		WPI; 2003-066697/06.
PI		N-PSDB; ABS57788.
XX		
DR		New polypeptide for treating or preventing diseases associated with an
DR		abnormal platelet-derived growth factor (PDGF) level, e.g. cell
XX		
PT		

PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 88-91; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)
CC beta mutant T672M
XX
SQ Sequence 1106 AA;
Query Match 99.8%; Score 5756; DB 6; Length 1106;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1104; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRLPGAMPALAKGELLLSLLLLLEPQISQGLVVTTPPGPELVNLVNSTFVLTCSGSAPV 60
Db 1 MRLPGAMPALAKGELLLSLLLLLEPQISQGLVVTTPPGPELVNLVNSTFVLTCSGSAPV 60
QY 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCHTNDSRGLETDERKRLYIFV 120
Db 61 VWERMSQEPPOEMAKAQDGTFSVLTLTNLTGLDTGEYFCHTNDSRGLETDERKRLYIFV 120
QY 121 PDPTVGFPLNDAAELFIFLTEITEITIPCRVTDPOLVTLHEKKGDVALPVYPDHORGF 180
Db 121 PDPTVGFPLNDAAELFIFLTEITEITIPCRVTDPOLVTLHEKKGDVALPVYPDHORGF 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
Db 241 EVVNFEWTPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTGTYTCNVTESVNDH 300
QY 301 ODEKAINITWVESGYRLLGEVGLQFAELHRSRTLQVVEAYPPPTVLWFKDNRITLGDS 360
Db 301 ODEKAINITWVESGYRLLGEVGLQFAELHRSRTLQVVEAYPPPTVLWFKDNRITLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480
QY 481 TYWEEQEFEVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
Db 481 TYWEEQEFEVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILIMLWQKPRYRIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYRIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSHLGSP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSHLGSP 660
QY 661 HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720

Db 661 HLNVVNLLGACMKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFEIRPPFSQLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
Db 1021 YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEPQLELQV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106
RESULT 12
ABO84677
ID ABO84677 standard; protein; 1107 AA.
XX
AC ABO84677;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP20-018.1.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
DR N-PSDB; ABD32963.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 18; seqid 706; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10

CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells(comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1107 AA;

Query Match 99.6%; Score 5745.5; DB 8; Length 1107;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1104; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MRLPGAMPALALKGELLSSLLLLLEPQISQGLVTPPGPELVNVNSTFVLTCSGAPV 60
Db 1 MRLPGAMPALALKGELLSSLLLLLEPQISQGLVTPPGPELVNVNSTFVLTCSGAPV 60
QY 61 VVERMSQEPPOEMAKAQDGFSSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Db 61 VVERMSQEPPOEMAKAQDGFSSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120
QY 121 PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDQQLVTLHEKKGDVALPVPYDHQGFPS 180
Db 121 PDPTVGFLPNDAAELFIFLTEITEITIPCRVTDQQLVTLHEKKGDVALPVPYDHQGFPS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVVNFEWTPYPRKE-SGRLVEPVTDFLLDMPYHIRSILHIPSAALEDSGTYTCNVTVSVND 299
Db 241 EVVNFEWTPYPRKEVIGRLVEPVTDFLLDMPYHIRSILHIPSAALEDSGTYTCNVTVSVND 300
QY 300 HQDEKAINITVVESGYVRLGEGVGTQFAELHRSRTLQVVEAYPPPTVLWFKDNRFTLGD 359
Db 301 HQDEKAINITVVESGYVRLGEGVGTQFAELHRSRTLQVVEAYPPPTVLWFKDNRFTLGD 360
QY 360 SSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRV 419
Db 361 SSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRV 420
QY 420 LELSESHPDSSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPPTLLGNSSSEESQLETN 479
Db 421 LELSESHPDSSGEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPPTLLGNSSSEESQLETN 480
QY 480 VTYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVTVISAIL 539
Db 481 VTYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVTVISAIL 540

QY 540 ALVVLTIISLIILIMLWQKKPRYRIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPRDQ 599
Db 541 ALVVLTIISLIILIMLWQKKPRYRIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPRDQ 600
QY 600 LVLGRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLG 659
Db 601 LVLGRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLG 660
QY 660 PHLVNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHHSKRRPPPSAELYSNA 719
Db 661 PHLVNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHHSKRRPPPSAELYSNA 720
QY 720 LPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGVKYADIESSNYMAPYDNYV 779
Db 721 LPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGVKYADIESSNYMAPYDNYV 780
QY 780 PSAPERTCRATLINESPVLSDLVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKL 839
Db 781 PSAPERTCRATLINESPVLSDLVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKL 840
QY 840 VKICDFGLARDIMRDSNYISKSTFELPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTL 899
Db 841 VKICDFGLARDIMRDSNYISKSTFELPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTL 900
QY 900 GGTYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLLE 959
Db 901 GGTYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQVLVLLLE 960
QY 960 RLLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPDLTSSVLYTAVQPNEGDN 1019
Db 961 RLLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPDLTSSVLYTAVQPNEGDN 1020
QY 1020 DYIIPDPKPKEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQ 1079
Db 1021 DYIIPDPKPKEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQ 1080
QY 1080 VEPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1081 VEPEPELEQLPDSGCPAPRAEAEDSFL 1107
RESULT 13
AAP90646
ID AAP90646 standard; protein; 1106 AA.
XX
AC AAP90646;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-OCT-1989 (first entry)
XX
DE Human platelet-derived growth factor receptor.
XX
KW Human platelet derived growth factor receptor;
KW agonist and antagonist drugs; wound healing; prevents atherosclerosis;
KW cancer; genetic disorders; antibodies.
XX
OS Homo sapiens; (human).
XX
FH Key Location/Qualifiers
FT Region 45. .47
FT Region 89. .91
FT Region 103. .105
FT Region 215. .217
FT Region 230. .232
FT Region 292. .294
FT Region 307. .309
FT Region 354. .356
FT Region 371. .373
FT Region 468. .470
FT Region 479. .481
FT Domain 531. .555

PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX N-PSDB; AAS84940.
DR New isolated polynucleotide and encoded polypeptides, useful in
DR diagnostics, forensics, gene mapping, identification of mutations
DR responsible for genetic disorders or other traits and to assess
DR biodiversity.
XX Claim 20; SEQ ID NO 51112; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1089 AA;
SQ Query Match 98.1%; Score 5657.5; DB 4; Length 1089;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 17; Gaps 1;
QY 1 MRLPGAMPALAKGELLLSLLSLLLEFPQISQGLVWTPPGPELVNVSSTFVLTCGSAVP 60
DB 1 MRLPGAMPALAKGELLLSLLSLLLEFPQISQGLVWTPPGPELVNVSSTFVLTCGSAVP 60
QY 61 VWERMSQEPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
DB 61 VWERMSQEPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
QY 121 PDPTVGFLPNDABELFIFLTFEITIPCRVTDPLQVVTLEHKKGDVALPVPYDHQGES 180
DB 121 PDPTVGFLPNDABELFIFLTFEITIPCRVTDPLQVVTLEHKKGDVALPVPYDHQGES 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
DB 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
QY 241 DVNFEWTPYRKESGRLVEPVTDFLLDMPYHRSILHIPSABELEDSTGTYTCNVTVSNVNDH 300
DB 241 EVNFEWTPYRKESGRLVEPVTDFLLDMPYHRSILHIPSABELEDSTGTYTCNVTVSNVNDH 300
QY 301 QDEKAINITVVEGYSVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTLVLFKDNRTILGDS 360
DB 301 QDEKAINITVVEGYSVRLLEGEVGTLOFAELHRSRTLOVVFAYPPPTLVLFKDNRTILGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFOLQINVPVRVL 420
DB 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFOLQINVPVRVL 420
QY 421 ELSHSDSDSGEQTVRCRGRMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480

Db 421 ELSHSDSDSGEQTVRCRGRMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEQEFVSTLRLQHVDRPLSVRCTLRNAVGDQTQEVIVVPHSLPFKVVVISAILA 540
DB 481 TYWEEQEFVSTLRLQHVDRPLSVRCTLRNAVGDQTQEVIVVPHSLPFKVVVISAILA 540
QY 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHXYIVDPMQLPYDSTWELPRDQL 600
DB 541 LVVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHXYIVDPMQLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSELKIMSHLGP 660
DB 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSELKIMSHLGP 660
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHHSKRRPPSAELYSNAL 720
DB 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHHSKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLTGESDGGYNDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780
DB 721 PVGLPLPSHVSLTGESDGGYNDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLVMDLVGFYSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
DB 781 SAPERTCRATLINESPVLVMDLVGFYSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
DB 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER 960
DB 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER 960
QY 961 LLGEGYKKYQOVDEEFLRSDHPAILRQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
DB 961 LLGEGYKKYQ-----QARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1003
QY 1021 YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPEQLEQV 1080
DB 1004 YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPEQLEQV 1063
QY 1081 EPEPELEQLPDGCGPAPRAEADSFL 1106
DB 1064 EPEPELEQLPDGCGPAPRAEADSFL 1089

Search completed: March 11, 2005, 07:07:45
Job time : 134.495 secs

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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:07:56 ; Search time 34.2633 Seconds
(without alignments)
3105.821 Million cell updates/sec

Title: US-10-027-400-4
Perfect score: 5766
Sequence: 1 MRLPGAMPALALKGELLLLS.....EQLPDSGCPAPRAEADSFL 1106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1 PFHUGB	platelet-derived g
2	4972	86.2	1098	1 PFMSRB	platelet-derived g
3	2403	41.7	1048	2 T30815	platelet-derived g
4	2351.5	40.8	1089	1 PFHUGA	platelet-derived g
5	2319	40.2	1087	2 I51552	platelet-derived g
6	2304	40.0	1088	1 PFRTGA	platelet-derived g
7	2271.5	39.4	1089	1 S33727	platelet-derived g
8	2115	36.7	499	2 S33766	platelet-derived g
9	1432.5	24.8	980	1 TVCTMD	macrophage colony-
10	1425	24.7	978	1 A49814	protein-tyrosine k
11	1421.5	24.7	941	1 TVMVMD	protein-tyrosine k
12	1401.5	24.3	960	1 JN0677	protein-tyrosine k
13	1400.5	24.3	976	1 TVHUKT	protein-tyrosine k
14	1384.5	24.0	977	2 I45877	protein-tyrosine k
15	1382.5	24.0	975	1 TVMSKT	protein-tyrosine k
16	1382	24.0	978	2 S16385	macrophage colony-
17	1370.5	23.8	972	1 TVHJMD	macrophage colony-
18	1355.5	23.5	976	1 TVMSMD	macrophage colony-
19	1327	23.0	954	2 I51703	c-kit-related kina
20	1274	22.1	975	2 T30816	macrophage colony-
21	1138	19.7	1333	2 I78875	receptor tyrosine
22	1138	19.7	1379	2 JC4954	vascular endotheli
23	1133.5	19.7	1336	2 I60598	Fit-1 tyrosine kin
24	1131.5	19.6	457	2 S44269	platelet-derived g
25	1115	19.3	1348	2 S51656	vascular endotheli
26	1105	19.2	1363	2 I58375	protein-tyrosine k
27	1100.5	19.1	1330	2 S49010	embryonic receptor
28	1099.5	19.1	1338	2 S09982	protein-tyrosine k
29	1095	19.0	1000	2 S18827	Flt3 protein - mou

30	1084	18.8	1298	2 A48999	protein-tyrosine k
31	1077	18.7	992	2 A39931	protein-tyrosine k
32	1067.5	18.5	993	2 A36873	protein-tyrosine k
33	1050	18.2	1356	2 JC1402	protein-tyrosine k
34	1010	17.5	1367	2 A41228	protein-tyrosine k
35	993.5	17.2	790	1 FOMVHZ	gag-kit polyprotei
36	825	14.3	822	2 S54846	fibroblast growth
37	824	14.3	797	2 S38579	fibroblast growth
38	824	14.3	822	2 A45081	fibroblast growth
39	823.5	14.3	812	1 A36477	fibroblast growth
40	819.5	14.2	832	2 JH0393	fibroblast growth
41	818.5	14.2	822	1 TVMSFG	fibroblast growth
42	816.5	14.2	822	2 I49289	fibroblast growth
43	816	14.2	822	2 A41794	keratinocyte growt
44	815.5	14.1	821	1 TVHUF2	fibroblast growth
45	813.5	14.1	814	1 A39752	fibroblast growth

ALIGNMENTS

RESULT 1

PFHUGB

platelet-derived growth factor receptor beta precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text change 09-Jul-2004

C:Accession: A28206; A31195; A38268; A31925; B31925; C31925

R:Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988

A>Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f

A:Reference number: A28206; MUID:88217915; PMID:2835772

A:Accession: A28206

A:Molecule type: mRNA

A:Residues: 1-1106 <GRO>

A:Cross-references: UNIPROT:P09619; GB:J03278; NID:gl89731; PIDN:AAA60049.1; PID:gl89732

R:Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet

Mol. Cell. Biol. 8, 3476-3486, 1988

A>Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re

A:Reference number: A31195; MUID:89096941; PMID:2850496

A:Accession: A31195

A:Molecule type: mRNA

A:Residues: 1-240, 'D', 242-1106 <CLA>

A:Cross-references: GB:M21616; NID:gl89729; PIDN:AAA36427.1; PID:gl89730

R:Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: A38268

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 828-884 <PAR>

R:Roberts, W.M.; Look, A.T.; Roussel, M.F.; Sherr, C.J.

Cell 55, 655-661, 1988

A>Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.

A:Reference number: A90908; MUID:89028677; PMID:2846185

A:Accession: A31925

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 676-727 <ROB>

A:Accession: B31925

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 901-932 <RO2>

A:Accession: C31925

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1047-1106 <RO3>

C:Comment: The extracellular domain is predicted to include five immunoglobulin-like dom

C:Genetics:

A:Gene: GDB:PDGFRB

A:Cross-references: GDB:120710; OMIM:173410

A:Map position: 5q31-5q32

QY	824	HRDLAARNVLICGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTL	883
Db	819	HRDLAARNVLICGKLVKICDFGLARDIMHDSNYISKGSTFLPLKWMAPESIFHNLYTTL	878
QY	884	SDVWSFGILLWEIFTLGTPYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEE	943
Db	879	SDVWSYGILLWEIFTLGTPYPDLPMNELFYSPLKRGYRMAKPAHASDEVYEIMKRCWDE	938
QY	944	KFEIRPPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLD	1003
Db	939	TFEKRPDFSFLVHCVGDMLTDSYKKYSQVNETFLKSDHPAVARTKRLSSPFIANPAF	998
QY	1004	TSSVLY-----TAVQNEGD-----NDYIILPLDPKPDE	1031
Db	999	GPSLVGLSDFDPYNQNTRRFRNEAEVQEGVTSFNEYIIPIDPKPE	1046
RESULT 4			
PFHUGA			
platelet-derived growth factor receptor alpha precursor - human			
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)			
C;Species: Homo sapiens (man)			
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004			
C;Accession: A40162; A32941			
R;Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle, W.; Kraus, M.; Pierce, J			
Science 243, 800-804, 1989			
A;Title: Isolation of a novel receptor cDNA establishes the existence of two PDGF recept			
A;Reference number: A40162; MUID:89130149; PMID:2536956			
A;Accession: A40162			
A;Molecule type: mRNA			
A;Residues: 1-1089 <MATS>			
A;Cross-references: UNIPROT:P16234; GB:M21574; NID:g189733; PIDN:AAA96715.1; PID:g189734			
R;Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Helden, C.H.			
Proc. Natl. Acad. Sci. U.S.A. 86, 4917-4921, 1989			
A;Title: cDNA cloning and expression of the human A-type platelet-derived growth factor			
A;Reference number: A32941; MUID:89296915; PMID:2544881			
A;Accession: A32941			
A;Molecule type: mRNA			
A;Residues: 1-1089 <CLA>			
A;Cross-references: GB:M22734; NID:g189725; PIDN:AAA60048.1; PID:g189726			
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom			
C;Genetics:			
A;Gene: GDB:PDGFRA			
A;Cross-references: GDB:120267; OMIM:173490			
A;Map position: 4q11-4q12			
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;			
F;Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phosph			
F;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-1089/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>			
F;25-524/Domain: extracellular #status predicted <EXT>			
F;42-102/Domain: immunoglobulin homology <IMM1>			
F;143-191/Domain: immunoglobulin homology <IMM2>			
F;228-292/Domain: immunoglobulin homology <IMM3>			
F;428-503/Domain: immunoglobulin homology <IMM4>			
F;525-548/Domain: transmembrane #status predicted <TMM>			
F;549-1089/Domain: intracellular #status predicted <INT>			
F;591-957/Domain: protein kinase homology <KIN>			
F;599-607/Region: protein kinase ATP-binding motif			
F;42,76,103,179,353,359,458,468/Binding site: carbohydrate (Asn) (covalent) #status pred			
F;49-100,150-189,235-290,435-501/Disulfide bonds: #status predicted			
F;627/Active site: Lys #status predicted			
F;849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi			
Query Match			
Best Local Similarity 40.8%; Score 2351.5; DB 1; Length 1089;			
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;			
QY	8	PALALKGELL-LSLLLLLEPQISQGLVVTTPGPELVNLVNSSTFVLTCSGSA PVVWE-RM	65
Db	6	PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVQLNSSFSLRCFGESEVSWQYPM	61
QY	66	SQEPPEM-----AKAQDGTFSVLTLTNLTLGLDTGEYFCTHNSRGLGLED-ERKRLYIFV	120

Db	62	SEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIV	121
QY	121	PDPTVGFPLPNDABELFIFLTEITETIPCRVTDLPQLVTVLHEKKGDVALPVPYDHQRGFS	180
Db	122	PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSG--VVPASYDSRQGFN	179
QY	181	GIFEDRSYICKTTIGDREVSDAYVYVRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG	239
Db	180	GTFTVGPYICEATVGKKFQTFIPFNVYALKATSELDMEALKTVYKSGETIVVTCAVFN	239
QY	240	NDVVNFEWTPRKESGR--LVEPVTDFLLDMPYHIRSILHIPSAELEDSTGYTCNVTES	296
Db	240	NEVDLQWTPGGEVKGKITMLEEIKVPSIKLVY---TLTVPBATVKDSGDYECARQA	295
QY	297	VNDHQDEKAINITVVESGYVRLGEGVGTLQFAELHRSRTLQVVFAYPPPTVLWFKDNRT	356
Db	296	TREVEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNL	355
QY	357	LGDSSAGEIALSTRNVSETRYVSELTVRVKVAEAGHYTMRAFHEDAELVLSFQLOINVP	416
Db	356	LIENLT-EITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP	414
QY	417	VRVLESESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCRPRELPPPTLLGNS-----	469
Db	415	SSILDVDDHHGSTGGQTVRCTABGTPLPDIEWMICKOIKKCNNETSWTILANNVSNIT	474
QY	470	---SEESQLETNVTYWEEEQEFVVTSLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPH	526
Db	475	EIHSRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVAP	519
QY	527	SLPFKVVVISAILALVLTIIISLIILMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQ	586
Db	520	TLRSELTVAADVLLVIVIIISLIVLVWVKQPRYEIRWRVIESISPDGHEYIYVDPMQ	579
QY	587	LPYDSTWELPRDQLVGLRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ	646
Db	580	LPYDSRWEFPRDGLVGLGRVLGSAGFQGVVEGTAYGLSRSQPVVMKVAVKMLKPTARSSEKQ	639
QY	647	ALMSELKIMSHLGPLNVNLLGACTKGGPYIITEYCRYGLVDYLHRNKHTFLQHS	706
Db	640	ALMSELKIMTHLGPLNIVNLLGACTKSGPIYIITEYCFYGLVNVYLNKRDLSFLSHPE	699
QY	707	KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD	765
Db	700	K---PKKELDIFGLNPADESTRSYVILSFENNGYMDMKQADTQYVPMLEKEVSKYS	756
QY	766	IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH	824
Db	757	IQRSLYDRPASYYKKSMLDSEVKNLLSDNSEGLTLLDLSFTYQVARGMEFLASKNCVH	816
QY	825	RDLAARNVLICGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTL	884
Db	817	RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTL	876
QY	885	DVMSFGILLWEIFTLGTPYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK	944
Db	877	DVMSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE	936
QY	945	FEIRPPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLD	1004
Db	937	PEKRPSFYLSEIVENLLPGQYKKSYEKIHLDFLKSDDHPAVARNR-----VDS	984
QY	1005	SSVLYTAVQPN-----GNDYIILPL--DPKPEVADEGPLEGSPSLA	1045
Db	985	DNAYIGVTYKNEEDKLKWEGGLDEQRLSADSGYIILPDIDPVPEEEDLGKRNHRSSQT	1044
QY	1046	S---STLNEVNTSSTISCDSPLPQDEPEPEPQLEQVEPEPELEQLPDSGCPAPRAEAD	1103
Db	1045	SEESAETGSSSTF-----IKREDE-----TIE---DIDMDDIGIDSSDL-VED	1086
QY	1104	SFL	1106

Db 1087 SFL 1089

RESULT 5

I51552

platelet-derived growth factor A receptor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I51552

R;Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.

Dev. Genet. 14, 185-193, 1993

A;Title: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem

ion.

A;Reference number: I51552; MUID:93365089; PMID:8358864

A;Accession: I51552

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-1087 <JON>

A;Cross-references: UNIPROT:P26619; GB:M80798; NID:g214652; PIDN:AAA49929.1; PID:g214653

C;Genetics:

A;Gene: PDGFAR

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; growth factor receptor

F;43-103/Domain: immunoglobulin homology <IMM>

F;593-957/Domain: protein kinase homology <KIN>

F;601-609/Region: protein kinase ATP-binding motif

Query Match 40.2%; Score 2319; DB 2; Length 1087;

Best Local Similarity 44.7%; Pred. No. 9.8e-96;

Matches 505; Conservative 185; Mismatches 367; Indels 72; Gaps 21;

QY 7 MPALALKGELLSSLLLELPQ--ISQGLVVT--PPGPELVLVNSSTFVLTCSGSAPVVW 62

Db 2 MPAMRAS--LILGCLLIIGPWAILAENPLPTIFFDKDELVQALHSFTLKCTGESEVSW 58

QY 63 ERMSQEPPOE-----MAKAQDGTFSFVLTLTNLTLGLDTGEYFCTHNSRGLETD-ERKRL 116

Db 59 QNPNSNPEKQNVVIRSEENNSGLFVSILEVSDASAFDTGLTYCYNHTQTSESEIEGTDI 118

QY 117 YIFVPDPTVGLPNDAAELFIFLTEITEITPCRVTDPPQLVVTLHEKKGDVALVPYDQ 176

Db 119 YIYVPDPNPVPAPPGLFDHIIVVEEDESALVPCRTTDPSSSEVTLKNIESSRTVFAFYDSK 178

QY 177 RGFSGIFEDRSYICKTTIGDREVSDSDAYVYRLQVS-SINVSNAVQTVVRQENITLMC 235

Db 179 QGFAGNFPFGSYICETTSKNVYQTEPYILQTWKATHNISVEMEAPKTMFRAGETIAIDC 238

QY 236 IVIGNDVNFETWYPRKESGRVPEVPTDFLLDMPY-HIRSILHIPSAABLEDSGTYTCNV 294

Db 239 IVLNDEVVDLKWTPYQKQGVGIRNVEE--SKVPYQRLVYTLTLANATTEDSGEYEC 296

QY 295 ESVNDHQDEKAINITVWESGYVRLGEGVTLQFAELHRSRTLQVVFAYPPPTVLWFKDN 354

Db 297 HATLDNRVVVKTNITVHEKGFIDLEPMFGSEEFANLHEVKSFIVNLHAYPTPGLFWLKN 356

QY 355 RTLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAELVQLSFOLQIN 414

Db 357 RTLSENLT-EITTSIVTTKETRFQSKLIRAKEEDSGLYTLVAQNDRETKSYSFILQIK 415

QY 415 VPRVLELSHPD-SGEQTVRCRGRGMPQNPNIWSACRDLKRCPRPLPPTLLGNSSSEE 473

Db 416 VPALILELVKHHGASGEQTVGCLAKGMPVDDVEWLVCCKDIKRCNNDTLWSILATNGSEI 475

QY 474 SQLETNVTVWEEEQEFVSTLRLQHVDRPLSVRCRTLNRNAVQDQTQEVIVVPHSLPFKV 533

Db 476 SM----ETHQDEQ---IESQVTFKKIETMAIRCIKAKNELGVVARELKLVAPTLRSELT 528

QY 534 VISAILALVVLTIISLIILMLWQKPRYERWKVIESVSSDGHGYIYVDPMLPQYDSTW 593

Db 529 VAAAVLVLLVIVISLVLVLIWKQKPRYERWRVIESISPDGHEXYIYVDPMLPYDSRW 588

QY 594 ELPRDQLVGLRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELK 653

Db 589 EFPRDGLVLGRILSGAFGKVVGEAAYGLSRSPQVMKVAVKMLKPTARSSSEKQALMSELK 648

QY 654 IMSHLGPHLVNVNLLGACTKGGPIYIITEYCRYGDLDVYLHRNKHFTLQHHSDKRRPPSA 713

Db 649 IMTHLGAHLNIVNLLGACTKSGPIYIITEYCFYGDLVNLYLHKNRDNFQSRHPEK---PKK 705

QY 714 ELYSNAL-PVGLPLPSHVSLTGESDGYNDMSKDESVDYVPMMDKMGVKYADIESSNYM 772

Db 706 DLDFGLNEADESTRSYVILSFENNGDYMMDKQADTMQYVPMLEMKEPSKYSDIQRSLYD 765

QY 773 APYDNYVPSAPERTCRATLINES-PVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARN 831

Db 766 RPAS--YKKKPLSEVKNILSDDGFEGLTVLDDLSTYQVARGMEFLASKNCVHRDLAARN 823

QY 832 VLICEGLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGI 891

Db 824 VLLAHGKIVKICDFGLARDIMHDSNVYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSFGI 883

QY 892 LLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPF 951

Db 884 LLWEIFSLGGTPYPMIVDSTFYNKIKSGYRMAKPDHATHEVYDIMVKWNSEPEKRPSF 943

QY 952 SOLVLLERLLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSVLYTA 1011

Db 944 RHLSDIVESLLPMYKRCYETVLHDFLKSDHPAVTR-----NRSDSDNSYIGVTY 993

QY 1012 VQPNE-----GNDYIIPDPKPPEVADEGPLEGSPSLASSTLNEVNTSST 1057

Db 994 KNEHKMKDRESGFEQRLSADSGYIIPDPIDPVSDE---SGKRNHRHSSQTSEESALET 1050

QY 1058 ISCDSPLEQDEPEPEPQLELQVEPEPELQLPDSGCPAPRAEAEDSFL 1106

Db 1051 GSSSSTFIKRDD-----ETIEDIMDDDIGIDSSDL-VEDSFL 1087

RESULT 6

PFRTGA

platelet-derived growth factor receptor alpha precursor - rat

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C;Accession: A34710; S33767; S25100

R;Lee, K.H.; Bowen-Pope, D.F.; Reed, R.R.

Mol. Cell. Biol. 10, 2237-2246, 1990

A;Title: Isolation and characterization of the alpha platelet-derived growth factor rece-

A;Reference number: A34710; MUID:90220609; PMID:2157969

A;Accession: A34710

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1088 <LEE>

A;Cross-references: UNIPROT:P20786; GB:M63837; NID:g202929; PIDN:AAA40743.1; PID:g202930

A;Note: in the authors' translation an additional residue, Val, is shown after position

R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Biochim. Biophys. Acta 1173, 294-302, 1993

A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and rece-

A;Reference number: S33764; MUID:93305723; PMID:8318539

A;Accession: S33767

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 33-149,'R',151-518,'T',520-523 <HER1>

A;Cross-references: EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID:g56864

A;Experimental source: strain Sprague Dawley

R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

submitted to the EMBL Data Library, July 1992

A;Description: Cross-species conservation in sequence and function of PDGF ligands and r

A;Reference number: S25096

A;Accession: S25100

A;Molecule type: mRNA

A;Residues: 33-149,'R',151-518,'T',520-523 <HER2>

A;Cross-references: EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID:g56864

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; glycoprotein; heterodimer; homodimer; phosphoprote

F;1-23/Domain: signal sequence #status predicted <SIG>

Db 334 DLVVEFEAYPKPEHQWIYMNRT--PTNRGEDYVKSNDQSNIRYVNELRLTRLKGTGGT 391

Qy 394 YTMRAFHEDAEVQLSFQLOINVPVRVLELSHPDSGEQTVRCRGRMPQPNIWSACRD 453

Db 392 YTFVLSNSDVASASVTFDYYNTKPEIL-----TYDRLMNGRLQCVAAGPEPTIDWYFCG 447

Qy 454 L-KRCPRELPPT-----LLGNSSEESQLETNVTYWEESQEFVSVTLRLQ 498

Db 448 AEQRCTVPVPVDVQIQNASVSPFGKLVQSSIDSSVFRHNGT----- 490

Qy 499 HVDRPLSVRCTLRNAVQDT-----QEVIVPHSLPFKVVVISAILALVLTIIIS 548

Db 491 -----VECKASNAVGSKSAFFNAFKGNSKEQIQPHTL-FTPLLIQFVVTAGLMGII- 541

Qy 549 LIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQLVLRGLTGS 608

Db 542 VMVLAYKYLQKPMYEVQWKVEEI--NGNNYVYIDPTQLPYDHKWEFFRNRLSFGKTLGA 599

Qy 609 GAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSELKIMSHLGPLHNVNLL 668

Db 600 GAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELVLSYLGNMHNVNLL 659

Qy 669 GACTKGGPIYITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNALPVGLPLPS 728

Db 660 GACTVGGPTLVITEYCCYGDLLNFLRRKRSFI--FSKQEEQADAALYKNLL----- 709

Qy 729 HVSLTGESDGYMDMSKDESVDYVPMMLDMKGDVKY-----ADIESNYMAPYDNYVPSAP 783

Db 710 HSK-----ESSCDSNEY---MDMKPGVSVVWPTKTKRRS---ARIDSYI---- 749

Qy 784 ERTCRATLINESPV-LSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLVKI 842

Db 750 ERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKI 809

Qy 843 CDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGT 902

Db 810 CDFGLARDIRNDSNYVVKGNARLPVKWMAPEISFNCVYTFESDVWSYGIFLMELFSLGSS 869

Qy 903 PYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLLERLL 962

Db 870 PYGMPVDSQFYKMIKEGFRMLSPHEAPAAIYEVMTCTWDADPLKRPFTFKQVVQVQVLEKQI 929

Qy 963 GEGYKKYQQVDEEFLRSDHPAILRSQARL 992

Db 930 SDSSKHIYNSLANCPNPENPVVVDHSVRV 959

RESULT 11

TMVMD

protein-tyrosine kinase (BC 2.7.1.112) fms precursor - feline sarcoma virus (strain McDo

C;Species: feline sarcoma virus

A;Note: host Felis sp. (cat)

C;Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: A00654

R;Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.

Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984

A;Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected ho

A;Reference number: A00654; MUID:84119469; PMID:6582485

A;Accession: A00654

A;Molecule type: DNA

A;Residues: 1-941 <HAM>

A;Cross-references: UNIPROT:P00545

C;Comment: This protein is synthesized as a gag-fms polyprotein.

C;Genetics:

A;Gene: fms

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; otein kinase

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-941/Product: protein-tyrosine kinase fms #status predicted <MAT>

F;24-509/Domain: extracellular #status predicted <EXT>

F;35-86/Domain: immunoglobulin homology <IMM1>

F;120-179/Domain: immunoglobulin homology <IMM2>

F;217-280/Domain: immunoglobulin homology <IMM3>

F;316-381/Domain: immunoglobulin homology <IMM4>

F;410-484/Domain: immunoglobulin homology <IMM5>

F;510-534/Domain: transmembrane #status predicted <TMM>

F;535-941/Domain: intracellular #status predicted <INT>

F;577-915/Domain: protein kinase homology <KIN>

F;585-593/Region: protein kinase ATP-binding motif

F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted

F;45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #

F;613,630,776/Active site: Lys, Glu, Asp #status predicted

F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 24.7%; Score 1421.5; DB 1; Length 941;

Best Local Similarity 35.5%; Pred. No. 5.8e-56;

Matches 371; Conservative 155; Mismatches 347; Indels 171; Gaps 36;

Qy 19 LSLLLLEPQISQGL-VVTPPGPELVNLVNSSTFVLTCSGSAPVVWE-----RMSQEP 70

Db 6 LLVLLMATAWHAQGVPIQPSGPELVVEPGTTVTLRCVGVNGSVEMDGPISPHWNLDLDP 65

Qy 71 QEMAKAQDGTFFSSVLTLTNLTLGLDTGEYFCTH--NDSRGLETDERKRLYIFVPDPTVGFL 128

Db 66 -----SSILTTNNATFQNTGYTHCTEPGNRGGNAT-----IHLVVKDP----- 104

Qy 129 PNDAEELFIFLTEIT-----EITIPCRVTDPOLV--VTLHEKKGDVAL---PVPYDHQRG 178

Db 105 ---ARPWKVLAQEVTVLEGQDALLPCLLTDPALEAGVSLVRGRVLRQTNYSFSPWHG 161

Qy 179 F----SGIFEDRSYICKTTIGDREVSDDAYVY-YRLQVSS-INVSNAVQTVVRQGENIT 232

Db 162 FTIHKAKFIENHVYQCSARVGRVTSMGIWLKVKQDISGPATLLEPAELVRIQGEAAQ 221

Qy 233 LMCIVIGNDVVNFETWYPRKESGRLEVPEVPTDFLLDMPYHIRSILHIPSAELEDSTYTCN 292

Db 222 IVCSASNID-VNFDVSLRHGDTKLTISQQSDF-HDNRYQKVLTLNLDHVSFQDAGNYSCT 279

Qy 293 VTESVNDHQDEKAINITVVESGYVRLGGEVGTLOFAELHRSRTLVQVFEAYPP-PTVLWF 351

Db 280 ATNAWGNH--SASMVFRVVESAYSNLTSEQSLLOEVTVGEKVDLQVKVEAYPGLESFNW- 336

Qy 352 KDNRTLGDSSAGEIALSTRNVSET-RYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQ 410

Db 337 ---TYLGFPSDYQDKLDFVTIKDYRTYSTLSLPRLKRSSEGRYSFLARNAGGQNALTFE 393

Qy 411 LQINVP--VRV-LELSESHPDSGEQTVRCRGRMPQPNIWSACRD-LKRCPRELPPTLL 466

Db 394 LTLRYPPEVRVTMTLI-----NGSDTLCEASGYPPQPSVTWQCRSHTDRCDSESAGLVLE 448

Qy 467 GNSSEESQLETNVTYWEESQEFVV--STLRLOHVDRPLSVRCTLRNAVQDQTEV--- 521

Db 449 DSHSEVLSQVPF-----YEVIVHSLLAIGTLEHNRITYECRAFNSVGNSSQTFWPI 498

Qy 522 -----IVVPHSLPFKVVVISAILALVLTIIISLIILIMLWQKKPRYEIRWKVIESVSDG 576

Db 499 SIGAHTPLPDELLFTPVLLTC-MSIMALLLLLLLLLLLYKKYKQPKYQVRWKIIESY--EG 555

Qy 577 HEYIYVDDPMQLPYDSTWELPRDQLVLRGLTSGCAFQGVVEATAHGLSHSQATMKVAVKML 636

Db 556 NSYTFIDPTQLPYNEKWEFFPRNNLQFGKTLGTGAFGKVVEATAFGLGKEDAVLKVAVKML 615

Qy 637 KSTARSEKQALMSELKIMSHLGPLHNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRN 696

Db 616 KSTAHADEKEALMSELKIMSHLQHENIVNLLGACTHGGPVLVITEYCCYGDLLNFLRR- 674

Qy 697 KHTFLOHSDKRRPPSAELYSNALPVGLPLPS-HVSLTGESDGGYMDMSKDESVDYVPML 755

Db 675 -----QAE-----AMPGPSLSVGQDPEAGAGYKNIHLEK----- 703

Qy 756 DMKGDVKYADIESNYMAPYDNYVPSAPERTCRATLINES-----PVLSDMLV 804

Db 704 -----KYVRRDSGFSQGVDTYVEMRPVSTSSS---NDSFSEEDLGKEDGRPLELRDLL 754

Qy 805 GFSYQVANGMEFLASKNCVHRDLAARNVLICEGLVKICDFGLARDIMRDSNYISKGSTF 864

Db	755	HESSQAQGMFLASKNCIHRDVAARNVLLTSGRVAKIGDFGLARDIMNDSNIYIVKGNAR	814
QY	865	LPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTYPPELPMNEQFYNAIKRGYRMA	924
Db	815	LPVKWMAPESIFDCVYTVQSDVWSYGILLWEIFSLGLNPYPGILVNSKFYKLVKDGQYMA	874
QY	925	QPAHASDEIYEIMQKWEEKFEIRPPFSQVLVLLERLLGEGYKKYQQVDEEFLRSDHPA	984
Db	875	QPAFAPKNIYSIMQACWALEPTRRPTFQQICSLQK-----QAQED-----	915
QY	985	ILRSQARLPGFHGLRSPLDTSSVL 1008	
Db	916	-----RRVPNYTNL--PSSSSRL. 932	
RESULT 12			
JN0677			
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken			
N;Alternate names: tyrosine kinase receptor kit			
C;Species: Gallus gallus (chicken)			
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C;Accession: JN0677			
R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Sakurai, M			
Gene 128, 257-261, 1993			
A;Title: Cloning and expression of the chicken c-kit proto-oncogene.			
A;Reference number: JN0677; MUID:93292995; PMID:7685729			
A;Accession: JN0677			
A;Molecule type: mRNA			
A;Residues: 1-960 <SAS>			
A;Cross-references: UNIPROT:Q08156; DDBJ:D13225; NID:g303532; PIDN:BAA02506.1; PID:g3035			
A;Experimental source: brain			
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;			
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;			
rotein kinase			
F;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>			
F;314-380/Domain: immunoglobulin homology <IMM>			
F;573-916/Domain: protein kinase homology <KIN>			
F;581-589/Region: protein kinase ATP-binding motif			
F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)			
Query Match 24.3%; Score 1401.5; DB 1; Length 960;			
Best Local Similarity 34.9%; Pred. No. 4.6e-55;			
Matches 352; Conservative 161; Mismatches 368; Indels 127; Gaps 32;			
QY	3	LPGAMPALAKGELLLLSLLLLLEPQISQGLVVTPPGPELVLVNSSTFVLTCSGSAPVW	62
Db	1	MEGAHLAWELAHAVLLSL-----IPAGSVPHKESSLVNVKGBELRLKCNEEGPVTW	53
QY	63	ERMSQEPPOEMAKAQDGTFFSSVLTLTNLTLGLDTGEYFCTHNDSSRGLETDERKRLYIFVPD	122
Db	54	NFQNSDPSAKTRISNEKEWHT----KNATIRDIGRYEC---KSKGSIVNS---FYVFVKD	103
QY	123	PTVGFLPNDABELFIFLTEITEITIPCRVTDPPQLV-VTLHEKKGDVALPVVPYDH-----	175
Db	104	PNVFLVDS-----LIYGKEDSDILLVCPLTDDVLNFTLRKCDGK---PLPKNMTFIPNP	156
QY	176	-----QRGFSGIFEDRSYICKTTIGDREVDSDAYVYRLQVSSIN-----VSVNAV	221
Db	157	QKGIIIKNVQRSFKGCYQ-----CLAKHNGVEKISEHIF---LNVRPVHKALPVITLSKS	208
QY	222	QTVVRQGENITLMCIVIGND-VVNFETYPRKESGRVPEVPTDFLLDMPYHIRSILHIPS	280
Db	209	YELLKEGEFEFVTCIITDVDSSVKASWI---SYKSAIVTSKRNLDGYGERKLTNIRS	265
QY	281	AELEDSGYTCNVTESVNDHQDEKAINITWVESGYVRLGVEGTLQFAELHRSRTLQVVF	340
Db	266	VGVNDSGEFTCAENPFG--KTNATVTLKALAKGFVRLFATWNTTIDINAGQNGNLTVEY	323
QY	341	EAYP-PPTVLWFKDNRTLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAF	399
Db	324	EAYPKPKEEVWYMYNETLQNSSDHYVKFKT--VGNNSYTSELHLTRLKGTGGIYTFVFS	381

QY	400	HEDAEVQLSPQLQINVPVRVLELSESHPDSGEQTVRCRGRGMPQNPQNIWSACRDL-KRCP	458
Db	382	NSDASSVTFNVYVTKPEILTDM----LGNDILQCvatGFPAPTYWYFPCPGTEQRCL	437
QY	459	RELPTLLGNSSEESQLETNVTYWEEB-QEFE---VVSTLRQLQHVDRPLSVRCTLRNAV	514
Db	438	DS--PTI-----SPMDVKVSYTNSSVPSFERILVESTVNASMFKSTGTICCEASS--	485
QY	515	GQDTQEV-----VVPHSLPFKVVVISAILALVVLTIISLILIMLWQKKPRYEIRW	566
Db	486	NGDKSSVFENFAIKEQIRTHTL-FTPLLIAFGVAAGLMCII-VMLVVIYLOKPKYEVQW	543
QY	567	KVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQLVLGRTLGSAGFQVVEATAHGLSHSQ	626
Db	544	KVVEEI--NGNNYVYIDPTQLPYDHKWEFFRNRLSFGKTLGAGAFQVVEATAYGLFKSD	601
QY	627	ATMKVAVKMLKSTARSSKQALMSELKIMSHLGPLHNLVNVNLLGACTKGGPIYIITEYCRY	686
Db	602	AAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHINIVNLLGACTIGGPTLVITEYCCY	661
QY	687	GDLVDYLHRNKHFTL---QHHSKRRPPPSAELYSNALPVGLPLPSHVSLTGESDGGYMD	742
Db	662	GDLNLFRRKRKDSFICPKHEEHAE-----AAVYENLLHQAE-----TADAVNEYMD	708
QY	743	MSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVPSAPERTCRATLINESPVL	802
Db	709	MKPGVSYAVPPKADKRPVK-----SGSY-----TDQDVTLSMLEDELALDVED	753
QY	803	LVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLVKVICDFGLARDIMRDSNYISKGS	862
Db	754	LLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNVVVKGN	813
QY	863	TFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGTPVPPELPMNEQFYNAIKRGYR	922
Db	814	ARLPVKWMAPESIFNCVYTFESDVWSYGILLWELFSLGSSPVPMPVDSKFYKMIKEGYR	873
QY	923	MAQPAHASDEIYEIMQKWEEKFEIRPPFSQVLVLLERLLGEGYKKY 970	
Db	874	MFSPECSPPEMYDIMKSCWDADPLQRPPTFKQIVOLIEQQQLSDNAPRVY 921	
RESULT 13			
TVHUKT			
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human			
N;Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit			
C;Species: Homo sapiens (man)			
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004			
C;Accession: S01426; PC1015; A41815; B41815; C41815; I37948; I56954; I54336			
R;Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Chen,			
EMBO J. 6, 3341-3351, 1987			
A;Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for an			
A;Reference number: S01426; MUID:88111521; PMID:2448137			
A;Accession: S01426			
A;Molecule type: mRNA			
A;Residues: 1-976 <YAR>			
A;Cross-references: UNIPROT:P10721; GB:X06182; NID:g34084; PIDN:CAA29548.1; PID:g34085			
R;Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.			
Chinese Biochem. J. 7, 618-629, 1991			
A;Title: Nucleotide sequece of two neighbouring fragments of human c-kit proto-oncogene			
A;Reference number: PC1015			
A;Accession: PC1015			
A;Molecule type: DNA			
A;Residues: 412-713 <HUW>			
A;Note: article in Chinese with English abstract			
R;Spritz, R.A.; Giebel, L.B.; Holmes, S.A.			
Am. J. Hum. Genet. 50, 261-269, 1992			
A;Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell g			
A;Reference number: A41815; MUID:92133600; PMID:1370874			
A;Accession: A41815			
A;Molecule type: DNA			
A;Residues: 579-583, 'L', 585-589 <SPR>			
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F;520-542/Domain: transmembrane #status predicted <TMM> F;543-975/Domain: intracellular #status predicted <INT> F;586-929/Domain: protein kinase homology <KIN> F;594-602/Region: protein kinase ATP-binding motif F;58-98,137-187,234-293,431-494/Disulfide bonds: #status predicted F;146,296,303,323,355,370,466,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;622,639,790/Active site: Lys, Glu, Asp #status predicted F;795,808/Binding site: magnesium (Asn, Asp) #status predicted		Query Match 24.0%; Score 1382.5; DB 1; Length 975; Best Local Similarity 34.5%; Pred. No. 3.2e-54; Matches 359; Conservative 169; Mismatches 353; Indels 161; Gaps 36;	
QY	17	LLLSLLLLLEPQISQGLVVTTPG-----PELVNVSSTFVLTCSGSAPVW----	62
Db	10	LLCVLLVLLRGQTATSPSPASPGEPSPSIHPAQSELIVEAGDTLSLTCIDPDFVRWTFK	69
QY	63	-----ERMSQEPQPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERK	115
Db	70	TYFNEMVENKKNWIEQKAEA-----TRTGTYT-----SNSNGLTSS-----	107
QY	116	LYIFVPDPTVGFPLPNDAAELFIFLTEITPCRVTDLPQLV-VTLHEKKGDVALP----	170
Db	108	IYVFVRDPAKLFLVG---LPLFGKEDSDALVRCPLTDPQVSNYSLIECDGK-SLPTDLT	162
QY	171	-VPYDHQRFSGSIFEDRSY--ICKTTIGDRE---VDSDAYVY-YRLQVSSIN-VSVNAVQ	222
Db	163	FVP-NPKAGITIKNVKRAYHRLCVRCAAQDGTWLHSDKFTLKVREAIKAIPIVSVVPETS	221
QY	223	TVVRQGENITLMCIVIGNDV---VNFEW--TYPRKESGRLVEPVTDFLLDMPYHIRSILH	277
Db	222	HLLKKGDTFTVVCTI--KDVSTSVNSMWLKNPQPQHIAQVKHNSWHRGDFNYERQETLT	279
QY	278	IPSAELEDSTYTCNVTESVNDHQDEKAINIT----VVESGYVRLGCEVGTLQFAELHRS	333
Db	280	ISSARVDDSGVMCYANNTFG-----SANVTTTLKVEKGFINISPVKNTTVFVTDGEN	333
QY	334	RTLQVVFAYPPPT-VLWFKDNRTLGDSSAGEIALSTRNVSETRYVSELTLRVKVVAEAG	392
Db	334	VDLVVEYEAYPEKPEHQWIYMNRT--SANKGKYVKSNDKSNIRYVYNQLRLTRLKGTEG	391
QY	393	HYTMRAFHEDAEVQLSFQLQINVPVRVLELSHSDSGEQTVRCRGRGMPQPNIIWSACR	452
Db	392	TYTFLVSNSDASAVTFNVVNTKPEIL---TYDRLINGMLQCVAEGFPEPTIDWYFCT	447
QY	453	DL-KRCPRELPT-----LLGNSSEESQLETNVTYWEEEQEFVVSTLRL	497
Db	448	GAEQRCITTPSPVDVQVQNVSVSPFGKLVVQSSIDSSVFRHNGT-----	491
QY	498	QHVDRPLSVRCTLRNAVQDQTQ-----EVIVVPHSLPFKVVVISAILALVLTIIISLII	551
Db	492	-----VECKASNDVGKSSAFFNFAFKEIQAHTL-FTPLLIGFVVAAGAMGII-VMV	541
QY	552	LIMLWQKPRYRIRWKVIESVSSDGHXYIYVDPMQLPYDSTWELPRDQLVGLRTLGSGAF	611
Db	542	LTYKYLQKPMYEVQWKVVEI--NGNNYVIDPTQLPYDHKWEFPRNRLSFGKTLGAGAF	599
QY	612	QGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGPHLNVVNLGAC	671
Db	600	GKVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNMNIVNLGAC	659
QY	672	TKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPPSAELYSNALPVGLPLPSHVS	731
Db	660	TVGGPTLVITEYCCYGDLLNFLRRKRDSFI--FSKQEEQAEALYKNLLHSTEP-----	711
QY	732	LTGESDGGYNDMSKDESVDYVPMLDKMGDVKYADIESSNYMAPYDNYVPSAPERTCRATL	791
Db	712	-SCDSSNEYMDMK--PGVSYV--VPTKTDKRRS-----ARIDSYI-----ERDVTPAI	754
QY	792	INESPV-LSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLVKICDFGLARD	850
Db	755	MEDDELALDLDLLSFSYQVAKAMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARD	814

QY	851	IMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTPYPPELPMN	910
Db	815	IRNDSNYVVGNGARLPPVKWMAPESIFSCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVD	874
QY	911	EQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLERLLGEGYKKKY	970
Db	875	SKFYKMIKEGFRMVSPPEHAPAEAMYDVNKTCDADPLKRPTFKQVVVQLIEKQISDSTKHII	934
QY	971	QQVDEEFLRSDHPAILRSQARL	992
Db	935	SNLANCNPENPVVVDHSVRV	956

Search completed: March 11, 2005, 07:49:21
Job time : 39.2633 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 05:13:43 ; Search time 144.611 Seconds
(without alignments)
3916.424 Million cell updates/sec

Title: US-10-027-400-4
Perfect score: 5766
Sequence: 1 MRLPCAMPALALKGELLLS.....EQLPDSGCPAPRAEADSFL 1106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1 PGDR HUMAN	P09619 homo sapien
2	5206.5	90.3	1103	2 Q6QNF3	Q6gnf3 canis famil
3	4976.5	86.3	1097	1 PGDR RAT	Q05030 rattus norv
4	4972	86.2	1098	1 PGDR_MOUSE	P05622 mus musculu
5	4957.5	86.0	1099	2 Q7TMR8	Q7tmr8 mus musculu
6	2403	41.7	1048	2 P79749	P79749 fugu rubrip
7	2351.5	40.8	1089	1 PGDS_HUMAN	P16234 homo sapien
8	2319	40.2	1087	1 PGDS_XENLA	P26619 xenopus lae
9	2317	40.2	1087	2 Q7ZY71	Q7zy71 xenopus lae
10	2304	40.0	1088	1 PGDS RAT	P20786 rattus norv
11	2303	39.9	1079	2 Q6E7G6	Q6e796 canis famil
12	2292.5	39.8	1089	1 PGDS_MOUSE	P26618 mus musculu
13	2292.5	39.8	1089	2 Q7TSJ3	Q7tsj3 mus musculu
14	2270	39.4	1087	2 Q9PUF6	Q9puf6 gallus gall
15	2210	38.3	1059	2 Q9DE49	Q9de49 brachydanio
16	2175.5	37.7	1062	2 Q8AXC7	Q8axc7 fugu rubrip
17	2142.5	37.2	1078	2 Q8AXC8	Q8axc8 fugu rubrip
18	2085	36.2	986	2 Q8UVR9	Q8uvr9 fugu rubrip
19	1538.5	26.7	790	2 Q8C4N3	Q8c4n3 mus musculu
20	1531	26.6	686	2 Q75WK5	Q75wk5 oryzias lat
21	1496	25.9	743	2 Q6P4H5	Q6p4h5 homo sapien
22	1445	25.1	976	2 Q8JFR5	Q8jfr5 brachydanio
23	1445	25.1	976	2 Q9W755	Q9w755 brachydanio
24	1432.5	24.8	980	1 KFMS FELCA	P13369 felis silve
25	1426	24.7	974	2 Q63702	Q63702 rattus ratt
26	1425	24.7	978	2 Q63116	Q63116 rattus norv
27	1424	24.7	978	1 KFMS FSVMD	P00545 feline sarc
28	1404.5	24.4	972	2 Q76II0	Q76ii0 callithrix
29	1404	24.3	975	1 KIT CANFA	Q97799 canis famil
30	1404	24.3	975	2 Q7YRV7	Q7yrv7 canis famil
31	1403	24.3	979	2 Q8WN23	Q8wn23 canis famil

32	1401.5	24.3	960	1 KIT_CHICK	Q08156 gallus gall
33	1401.5	24.3	972	2 Q99662	Q99662 homo sapien
34	1400.5	24.3	976	1 KIT HUMAN	P10721 homo sapien
35	1393.5	24.2	978	2 Q9XS93	Q9xs93 canis famil
36	1391.5	24.1	964	2 Q97744	Q97744 sus scrofa
37	1391.5	24.1	975	2 Q7TS86	Q7ts86 mus musculu
38	1391	24.1	977	1 KFMS_MOUSE	P09581 mus musculu
39	1390.5	24.1	964	2 Q9TQ00	Q9tqq0 sus scrofa
40	1390.5	24.1	964	2 Q9TQ01	Q9tqq1 sus scrofa
41	1390.5	24.1	975	2 Q6QJB8	Q6qjb8 mus musculu
42	1389.5	24.1	976	2 Q6IQ28	Q6iq28 homo sapien
43	1389.5	24.1	979	2 Q8C8K9	Q8c8k9 mus musculu
44	1388.5	24.1	975	2 Q6QJB7	Q6qjb7 mus musculu
45	1386	24.0	977	2 Q6NXV8	Q6nxv8 mus musculu

ALIGNMENTS

RESULT 1
PGDR HUMAN
ID PGDR_HUMAN STANDARD; PRT; 1106 AA.
AC P09619; Q8NSL4;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Beta platelet-derived growth factor precursor (EC 2.7.1.112)
DE (PDGF-R-beta) (CD140b antigen).
GN Name=PDGFRB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8217915; PubMed=2835772;
RA Gronwald R.G.K., Grant F.J., Haldeman B.A., Hart C.E., O'Hara P.J.,
RA Hagen F.S., Ross R., Bowen-Pope D.F., Murray M.J.;
RT "Cloning and expression of a cDNA coding for the human platelet-
derived growth factor receptor: evidence for more than one receptor
class."
RL Proc. Natl. Acad. Sci. U.S.A. 85:3435-3439(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89096941; PubMed=2850496;
RA Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,
RA Oestman A., Betsholtz C., Heldin C.-H.;
RT "cDNA cloning and expression of a human platelet-derived growth factor
(PDGF) receptor specific for B-chain-containing PDGF molecules."
RL Mol. Cell. Biol. 8:3476-3486(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 SEQUENCE OF 548-569 FROM N.A.
 MEDLINE=97429921; PubMed=9285559; DOI=10.1038/sj.onc.1201267;
 Chi K.D., McPhee R.A., Wagner A.S., Dietz J.J., Pantazis P.,
 Goustin A.S.;
 "Integration of proviral DNA into the PDGF beta-receptor gene in HTLV-
 I-infected T-cells results in a novel tyrosine kinase product with
 transforming activity.";
 Oncogene 15:1051-1057(1997).
 [5]
 SEQUENCE OF 1046-1106 FROM N.A.
 MEDLINE=89028677; PubMed=2846185; DOI=10.1016/0092-8674(88)90224-3;
 Roberts W.M., Look A.T., Roussel M.F., Sherr C.J.;
 "Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor
 genes.";
 Cell 55:655-661(1988).
 [6]
 SEQUENCE OF 33-47.
 PubMed=15340161; DOI=10.1110/ps.04682504;
 Zhang Z., Henzel W.J.;
 "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites.";
 Protein Sci. 13:2819-2824(2004).
 [7]
 AUTOPHOSPHORYLATION SITES.
 MEDLINE=89376563; PubMed=2550144; DOI=10.1016/0092-8674(89)90510-2;
 Kazlauskas A., Cooper J.A.;
 "Autophosphorylation of the PDGF receptor in the kinase insert region
 regulates interactions with cell proteins.";
 Cell 58:1121-1133(1989).
 [8]
 INTERACTION WITH APS.
 MEDLINE=99142932; PubMed=9989826; DOI=10.1038/sj.onc.1202326;
 Yokouchi M., Wakioka T., Sakamoto H., Yasukawa H., Ohtsuka S.,
 Sasaki A., Ohtsubo M., Valius M., Inoue A., Komiya S., Yoshimura A.;
 "APS, an adaptor protein containing PH and SH2 domains, is associated
 with the PDGF receptor and c-Cbl and inhibits PDGF-induced
 mitogenesis.";
 Oncogene 18:759-767(1999).
 [9]
 CHROMOSOMAL TRANSLOCATION WITH TRIP11.
 MEDLINE=98043615; PubMed=9373237;
 Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;
 "Fusion of the platelet-derived growth factor receptor beta to a novel
 gene CEV14 in acute myelogenous leukemia after clonal evolution.";
 Blood 90:4271-4277(1997).
 [10]
 X-RAY CRYSTALLOGRAPHY (1.79 ANGSTROMS) OF 751-755 IN COMPLEX WITH
 PIK3R1, AND COMPARISON WITH NMR ANALYSIS.
 MEDLINE=21450159; PubMed=11567151; DOI=10.1107/S0907444901012434;
 Paupit R.A., Dennis C.A., Derbyshire D.J., Breeze A.L., Weston S.A.,
 Rowsell S., Murshudov G.N.;
 "NMR trial models: experiences with the colicin immunity protein Im7
 and the p85alpha C-terminal SH2-peptide complex.";
 Acta Crystallogr. D 57:1397-1404(2001).
 [11]
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1102-1106 IN COMPLEX WITH
 SLC9A3R1 AND PDGFRA.
 MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;
 Karthikeyan S., Leung T., Ladias J.A.A.;
 "Structural determinants of the Na+/H+ exchanger regulatory factor
 interaction with the beta 2 adrenergic and platelet-derived growth
 factor receptors.";
 J. Biol. Chem. 277:18973-18978(2002).
 -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
 tyrosine-protein kinase activity. Phosphorylates Tyr residues at
 the C-terminus of PTPN11 creating a binding site for the SH2
 domain of GRB2.
 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with
 APS.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: Involved in a form of chronic myelomonocytic leukemia
 (CMML) characterized by abnormal clonal myeloid proliferation and
 by progression to acute myelogenous leukemia (AML) through a
 chromosomal translocation t(5;12)(q33;p13) that involves PDGFRB
 and ETV6/TEL.
 CC -!- DISEASE: Involved in a acute myelogenous leukemia through a
 chromosomal translocation t(5;14)(q33;q32) that involves PDGFRB
 and TRIP11. The fusion protein may be involved in clonal evolution
 of leukemia and eosinophilia.
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
 receptor subfamily.
 CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
 CC
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 CC
 CC EMBL: J03278; AAA60049.1; -
 CC EMBL: M21616; AAA36427.1; -
 CC EMBL: U33172; AAC51675.1; -
 CC EMBL: BC032224; AAH32224.1; -
 CC PIR: A28206; PFHUGB.
 CC PDB: 1GQ5; X-ray; A=1102-1106.
 CC PDB: 1H90; X-ray; B=751-755.
 CC PDB: 1LWP; Model; A=600-962.
 CC Genew; HGNC:8804; PDGFRB.
 CC H-InvDB; HIX005310; -
 CC MIM; 173410; -
 CC GO; GO:0004992; F:platelet activating factor receptor activity; TAS.
 CC GO; GO:0005017; F:platelet-derived growth factor receptor act. .; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_c2.
 CC InterPro; IPR011009; Kinase like.
 CC InterPro; IPR00719; Prot_kinase.
 CC InterPro; IPR01824; RecepttyrkinsIII.
 CC InterPro; IPR01245; Tyr_pkinase.
 CC InterPro; IPR008266; Tyr_pkinase_AS.
 CC InterPro; IPR009134; VEGFR.
 CC Pfam; PF00047; ig; 2.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR01832; VEGFRECEPTOR.
 CC ProDom; PD000001; Prot_kinase; 2.
 CC SMART; SM00408; IGC2; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS50835; IG_LIKE; 2.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 CC 3D-structure; ATP-binding; Chromosomal translocation;
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Phosphorylation; Proto-oncogene; Receptor; Repeat; Signal;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 32 Beta platelet-derived growth factor
 FT CHAIN 33 1106 receptor.
 FT DOMAIN 33 531 Extracellular (Potential).
 FT TRANSMEM 532 556 Potential.
 FT DOMAIN 557 1106 Cytoplasmic (Potential).
 FT DOMAIN 600 962 Protein kinase.
 FT SITE 527 528 Breakpoint for translocation to form
 FT TRIP11-PDGFRB.
 FT NP_BIND 606 614 ATP (By similarity).
 FT BINDING 634 634 ATP (By similarity).
 FT ACT_SITE 826 826 By similarity.
 FT MOD_RES 751 751 Phosphotyrosine (by autocatalysis).
 FT MOD_RES 857 857 Phosphotyrosine (by autocatalysis).

QY 61 VWERMSQEPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Db 61 VWERLSQEPLOQWARTQDGTFFSSTLTNTVTLGLDTGEYFCTYKSGHGLEPDGRKRLYIFV 120

QY 121 PDPTVGFELPNDABELFIFLTFEITEITIPCRVTDLPQVVTLHEKGDVALPVYPDHQRGFS 180
Db 121 PDPTMGFLPVDPEELFIFLTFEITEITIPCRVTDLPRLVVTLHEKKVDIPLPIPYDHQRGFS 180

QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GTFEDKTYVCKTTIGDKEVDSEAYVYSLQVSSINVSNAVQTVVRQGENITIMCIVTGN 240

QY 241 DVVNFETYPRKESGRLVEPVTDFLLDMPYHIRSILHIPSAELSDSGTYTCNVTVSNVNDH 300
Db 241 EVVNFETYPRMESGRLVEPVTDFLNVPSHIRSILHIPSAELGDSGTIYCNVSESVNDH 300

QY 301 ODEKAINITVYESGYVRLGEGVTLOFAELHRSRTLQVVFAYPPTVLWFKDNRTLGD 360
Db 301 RDEKSINVTVYESGYVRLGELDAVQFAELHRSRALQVVFAYPPTVVWFKDNRTLGD 360

QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAFHEDAEVQLSFQLOINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGYTMRAFHEDAEAQLSFQLOINVPVRVL 420

QY 421 ELSESHDPDSGQTVRCRGRMPQPNITWSACRDLKRCPRELPTLLGNSSEESQLETNV 480
Db 421 ELSESHDPASGQTVRCRGRMPQPHLTWSTCSDLKRCPRELPTLLGNSSEESQLETNV 480

QY 481 TYWEEEOEFVYSTLRLOHVDRLPLSVRCTLRNAVGQDTQEVIVVPHSLPFFKVVVISAILA 540
Db 481 TYWPEDQEFVYSTLRRLRRVDQPLSVRCTLHNLGHDMQEVTVVPHSLPFFKVVVISAILA 540

QY 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600

QY 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP 660

QY 661 HLNVVNLLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDDKRRPPSAELYSNAL 720
Db 661 HLNVVNLLGACTKGPIYIITEYCRYGDLVDYLHRNKHTFLQLCSDKRRPPSAELYSNAL 720

QY 721 PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780
Db 721 PAGLPLPSHVSILPGESDGGYMDMSKDESVDYVPMMLDMKGVKYADIESSNYMAPYDNYVP 780

QY 781 SAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 TAPERTCRATLINESPVLSTYDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840

QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFEIRPPFSQLVLLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFEIRPPFSQLVLLLER 960

QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSVLYTAVQPNEGDND 1020
Db 961 LLGEGYKKYQQVDEEFLRSDHPAVLRSQARLPGFPLRSPLDTSVLYTAVQPNEGDND 1020

QY 1021 YIIPLPDPKPEVADGPLEGSPSLASSTILNEVNTSSTICDSPLEPD--EPEPEPQLEL 1078
Db 1021 YIIPLPDPKPEVAD--GPLESSPSLASSTILNEVNTSSTICDSPLEPQEPPEPEPQPEP 1079

QY 1079 QVEPEPELEQLPDSGCPAPRAEAEDSFL 1106
Db 1080 QVWPEPPL----DSSCPGPRAEAEDSFL 1103

RESULT 3
PGDR RAT
ID PGDR RAT STANDARD; PRT; 1097 AA.
AC Q05030; Q8R406; Q925F7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE (PDGF-R-beta).
GN Name=Pdgfrb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Wang Y., Culty M.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 35-533 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;
RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
RT "Conservation in sequence and affinity of human and rodent PDGF
ligands and receptors.";
RL Biochim. Biophys. Acta 1173:294-302(1993).
RN [3]
RP SEQUENCE OF 528-1090 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21359359; PubMed=11346654; DOI=10.1074/jbc.M102995200;
RA Okuyama H., Shimahara Y., Kawada N., Seki S., Kristensen D.B.,
RA Yoshizato K., Uyama N., Yamaoka Y.;
RT "Regulation of cell growth by redox-mediated extracellular proteolysis
of platelet-derived growth factor receptor beta.";
RL J. Biol. Chem. 276:28274-28280(2001).
CC -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
tyrosine-protein kinase activity. Phosphorylates Tyr residues at
the C-terminus of PTPN11 creating a binding site for the SH2
domain of GRB2 (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
receptor subfamily.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.

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CC EMBL; AY090783; AAM09098.1; -.
CC EMBL; Z14119; CAA78489.1; -.
CC EMBL; AF359356; AAK43716.1; -.
CC PIR; S33766; S33766.
CC HSSP; P17948; IQSV.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001824; RecepttyrkinsIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR008266; Tyr_pkinase_As.
CC InterPro; IPR009134; VEGFR.
CC Pfam; PF00047; ig; 3.
CC Pfam; PF00069; Pkinase; 1.
CC PRINTS; PR01832; VEGFRECEPTOR.

DR	ProDom; PD000001; Prot_kinase; 2.	
DR	SMART; SM00408; IGc2; 1.	
DR	SMART; SM00219; TyrKc; 1.	
DR	PROSITE; PS50835; IG LIKE; 3.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.	
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;	
KW	Receptor; Repeat; Signal; Transferase; Transmembrane;	
KW	Tyrosine-protein kinase.	
FT	SIGNAL	1 31
FT	CHAIN	32 1097
FT	DOMAIN	32 532
FT	TRANSMEM	533 555
FT	DOMAIN	32 119
FT	DOMAIN	128 209
FT	DOMAIN	213 308
FT	DOMAIN	415 523
FT	DOMAIN	599 961
FT	NP_BIND	605 613
FT	ACT_SITE	825 825
FT	BINDING	633 633
FT	DISULFID	53 99
FT	DISULFID	148 189
FT	DISULFID	234 290
FT	DISULFID	435 507
FT	MOD_RES	750 750
FT	MOD_RES	856 856
FT	CARBOHYD	44 44
FT	CARBOHYD	88 88
FT	CARBOHYD	102 102
FT	CARBOHYD	214 214
FT	CARBOHYD	291 291
FT	CARBOHYD	306 306
FT	CARBOHYD	353 353
FT	CARBOHYD	370 370
FT	CARBOHYD	444 444
FT	CARBOHYD	467 467
FT	CARBOHYD	478 478
SQ	SEQUENCE	1097 AA; 122827 MW; 5E6540FA0C5CF22B CRC64;
Query Match 86.3%; Score 4976.5; DB 1; Length 1097;		
Best Local Similarity 85.9%; Pred. No. 4.8e-291;		
Matches 950; Conservative 69; Mismatches 78; Indels 9; Gaps 2;		
Qy	1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVTPPGPELVNVSTFVLTCSGAPV	60
Db	1 MGLPEVMPASVLRGQLLLF-VLLLLGPQISQGLVITPPGPEFVLNISSTFVLTCS	59
Qy	61 VWERMSQEPPOBMAKAQDGTFFSSVLTTLNLTGLDTGEYFCTHNDNRGLTDERKRLYIFV	120
Db	60 MWEQMSQVPWQEAAMNQDGTFFSSVLTTLNVTGGDTGEYFCVYNNNSLGPSELSE	119
Qy	121 PDPTVGFLPNDAELFIFLITEITPCRVTPDQPLVTLHEKKGVDVALPVYPDHORGS	180
Db	120 PDPTMGFLPMSEDLFIFVTDVTETPCRVTPDQPLEVTLHEKKVDIPLHVPYDHQRFI	179
Qy	181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLNCIVIGN	240
Db	180 GTFEDKTYICKTTIGDREVDSDTYVYVLSQVSSINVSNAVQTVVRQGESITIRCIVMGN	239
Qy	241 DVNFEWTPRKESGRLEVPVTDFLDMPYHRSILHIPSAALEDSGTYTCNVTESVNDH	300
Db	240 DVNFFQWTPRMKSGRLVEPVTDYLFQVPSRIGSILHIPTAELSDSGTYTCNVSVSNDH	299
Qy	301 QDEKAINITVVEGYSVRLLEGEVGTLOFABELHRSRTLQVWFEAYPPPTVLFKDNRTLGD	360
Db	300 GDEKAINVTIENGYSVRLLETTLEDVQIAELHRSRTLQVWFEAYPTPSVLWFKDNRTLGD	359

Qy	361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQIQINVPVRVL	420
Db	360 SAGELVLSSTRNVSETRYVSELTLVRVKVSEAGYYTMRAFHADDQVLSFKLQVNVVPVRVL	419
Qy	421 ELSESHPDGEGQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSSEESQLETNV	480
Db	420 ELSESHPANGEQILRCRGRGMPQPNVTWSTCRDLKRCPRKLSPTPLGNSSKEESQLETNV	479
Qy	481 TYWEEEOQEFVYSTLRLOHVDRLPSVRCCTLRNAVGDQTQEVIVPHSLPFKVVVISAILA	540
Db	480 TFWEEDQEVVYSTLRLRHVDQPLSVRCMLQNSMGRDSQEVTVPHSLPFKVVVISAILA	539
Qy	541 LVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGHHEYIYVDPMLQPYDSTWELPRDQL	600
Db	540 LVVLTVISLIILIMLWQKPRYEIRWKVIESVSSDGHHEYIYVDPVQLPYDSTWELPRDQL	599
Qy	601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	660
Db	600 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	659
Qy	661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLRHNKHTFLQHSDDKRRPPSAELYSNAL	720
Db	660 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLRHNKHTFLQRHSHKHCFFSTELYSNAL	719
Qy	721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESNMYMAPYDNYVP	780
Db	720 PVGLSLPSHLNLTGESDGGYMDMSKDESVDYVPMLDMKGHIKYADIESNMYMAPYDNYVP	779
Qy	781 SAPERTCRATLINESPVLVSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Db	780 SAPERTYRATLINDSPVLSYTDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	839
Qy	841 KICDFGLARDIMRDSNYISKSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	900
Db	840 KICDFGLARDIMRDSNYISKSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	899
Qy	901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER	960
Db	900 GTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIRPPFSQLVLLER	959
Qy	961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQPNEGND	1020
Db	960 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGLHSLRSPDLTSSVLYTAVQPNETDND	1019
Qy	1021 YIILPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEQDEPEPEPQLELQV	1080
Db	1020 YIILPDPKPDAADEGLLESPSLASSTLNEVNTSSTISCDSPLEQDEP-----QA	1071
Qy	1081 EPEPELEQLPDSGCPAPRAEADSFL	1106
Db	1072 EPEAQLEQPDGSGCPGLAEADSFL	1097
RESULT 4		
PGDR MOUSE		
ID	PGDR MOUSE	STANDARD;
AC	P05622;	PRT; 1098 AA.
DT	01-NOV-1988 (Rel. 09, Created)	
DT	01-NOV-1988 (Rel. 09, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Beta platelet-derived growth factor precursor (EC 2.7.1.112)	
DE	(PDGF-R-beta).	
GN	Name=PDGfrb; Synonyms=PDGfr;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC	TISSUE= Fibroblast;	
RX	MEDLINE=87014762; PubMed=3020426;	
RA	Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O.,	
RA	Tremble P.M., Chen E.Y., Ando M.S., Harkins R.N., Francke U.,	

RA Fried V.A., Ullrich A., Williams L.T.;
RT "Structure of the receptor for platelet-derived growth factor helps
RL define a family of closely related growth factor receptors.";
CC Nature 323:226-232(1986).
CC -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
CC tyrosine-protein kinase activity. Phosphorylates Tyr residues at
CC the C-terminus of PTPN11 creating a binding site for the SH2
CC domain of GRB2 (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with
CC APS (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04367; CAA27882.1; --
DR PIR; A25742; PFMSRB.
DR MGD; MGI:97531; Pdgfrb.
DR GO; GO:0004871; F:signal transducer activity; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.
DR GO; GO:0007165; P:signal transduction; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 31
FT CHAIN 32 1098 Beta platelet-derived growth factor
FT receptor.
FT DOMAIN 32 530 Extracellular (Potential).
FT TRANSMEM 531 555 Potential.
FT DOMAIN 556 1098 Cytoplasmic (Potential).
FT DOMAIN 33 119 Ig-like C2-type 1.
FT DOMAIN 128 209 Ig-like C2-type 2.
FT DOMAIN 213 308 Ig-like C2-type 3.
FT DOMAIN 415 523 Ig-like C2-type 4.
FT DOMAIN 599 961 Protein kinase.
FT NP_BIND 605 613 ATP (By similarity).
FT BINDING 633 633 ATP (By similarity).
FT ACT_SITE 825 825 By similarity.
FT DISULFID 53 99 Potential.
FT DISULFID 148 189 Potential.
FT DISULFID 234 290 Potential.
FT DISULFID 435 507 Potential.
FT MOD_RES 750 750 Phosphotyrosine (by autocatalysis) (By
FT similarity).

FT	MOD_RES	856	856	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CARBOHYD	44	44	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	88	88	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	102	102	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	214	214	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	291	291	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	353	353	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	370	370	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	444	444	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	467	467	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	478	478	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	1098 AA;	122805 MW;	8D391CAFAC3FC31D CRC64;

Query Match 86.2%; Score 4972; DB 1; Length 1098;
Best Local Similarity 85.4%; Pred. No. 9e-291;
Matches 945; Conservative 76; Mismatches 77; Indels 8; Gaps 2;

QY	1	MRLPGAMPALAKGELLLSLLLELPQISQGLVVTTPGPELVNVSTFVLTCSGSAPV	60
Db	1	MGLPGVIPALVLRGQ-LLLSVLWLLGPQTSRGLVITPPGPEFVLNISFVLTCSGSAPV	59
QY	61	VWERMSQEPPOEMAKAQDGTFFSVLTLTNLTGLDTGEYFCHNDSRGLETDERKRLYIFV	120
Db	60	MWEQMSQVPWQEAAMNQDGTFFSVLTLTNVTGGDTGEYFCVYNNVSLGPELSERKRIYIFV	119
QY	121	PDPTVGFPLNDAAELFIFLTFEITETIPCRVTDLPQLVVTLHEKKGDVALPVYPYDHQGRFS	180
Db	120	PDPTMGFLPMDSEDLFIFVTDVTETIPCRVTDLPQLVTLHEKKVDIPLHVPYDHQGRFT	179
QY	181	GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Db	180	GTFEKTYICKTTIGDREVSDTYVYVSLQVSSINVSNAVQTVVRQGESITIRCIVMGN	239
QY	241	DVNVFEWTPYRKESGRVPEVTDFLDMPYHIRSILHIPSAELEDSTGYTCNVTESVNDH	300
Db	240	DVNVFQWTPYPRMKSRLVEPVDYLVFGVPSRIGSILHIPTAELSDSTGYTCNVSVSNDH	299
QY	301	QDEKAINITVVESGYVRLGEGVTLPFAELHRSRTLVVFEAYPPPTVLWFKDNRTLGD	360
Db	300	GDEKAINISVIENGYVRLLETGLGVIEAELHRSRTLVRVFEAYPMPVSLWLNKDNRTLGD	359
QY	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDEAVQLSFQLQINVPVRL	420
Db	360	GAGELVSTRNMSETRYVSELTLVRVKVSEAGYTMRAFHEDEDEQLSFKLQVNVVPRVL	419
QY	421	ELSESHDPSGEQTVRCRGRGMPQNIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Db	420	ELSESHPANGEQTIRCRGRGMPQNVWTSTCRDLKRCPRKLSPTPLGNSSEESQLETNV	479
QY	481	TYWEEEOEFVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILA	540
Db	480	TFWEEDQIEYVWSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLPFKVVVISAILA	539
QY	541	LVVLTITSLIILMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPRDQL	600
Db	540	LVVLTVISLIILMLWQKKPRYEIRWKVIESVSSDGHYIYVDPVQLPYDSTWELPRDQL	599
QY	601	VLGRTLGSAGFQVWEATAHGLSHSOATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	660
Db	600	VLGRTLGSAGFQVWEATAHGLSHSOATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	659
QY	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDDRPPPSAEALYSNAL	720
Db	660	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSNKGHCPPSAEALYSNAL	719
QY	721	PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADISSNYMAPYDNYVP	780
Db	720	PVGFSPLPSHLNLTGESDGGYMDMSKDESIDYVPMLDMKGDIKYADIESPSYMAPYDNYVP	779
QY	781	SAPERTCRATLINESPVLVSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840

Db 780 SAPERTYRATLINDSPVLSYTDLVGFSYQVANGMDFLASKNCVHRDLAARNVLICEGKLV 839

QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900

Db 840 KICDFGLARDIMRDSNYISKGSTYLPKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 899

QY 901 GTPYPELPNNEQFYNAIKRGYRMAQPAHASDEIYIMQKCWEEKFEIRPPFSQLVLLER 960

Db 900 GTPYPELPNNDQFYNAIKRGYRMAQPAHASDEIYIMQKCWEEKFETRPPFSQLVLLER 959

QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPFGHGLRSPLDTSSVLYTAVQPNEGDND 1020

Db 960 LLGEGYKKYQQVDEEFLRSDHPAILRSQARFPGTHSLRSPLDTSSVLYTAVQPNESDND 1019

QY 1021 YIIPLPDPKPEVADGPLEGSPSLASSTLINEVNTSSTISCDSPLEPQDEPEPEPQLELQV 1080

Db 1020 YIIPLPDPKPDVADEGLPEGSPSLASSTLINEVNTSSTISCDSPLELQEEFQ-----QA 1072

QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

Db 1073 EPEAQLEQPQDSGCGPLAEADSFL 1098

RESULT 5

Q7TMR8 PRELIMINARY; PRT; 1099 AA.

AC Q7TMR8;

DT 01-OCT-2003 (TReMBLrel. 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Platelet derived growth factor receptor, beta polypeptide.

GN Name=Pdgfrb;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;

RA Strausberg R.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-

CC 1/PDGF receptor subfamily.

DR EMBL; BC055311; AAH5311.1; -.

DR HSSP; P11362; 1FGI.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0016301; F:kinase activity; IMP.

DR GO; GO:0004871; F:signal transducer activity; IDA.

DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.

DR GO; GO:0007165; P:signal transduction; IDA.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG c2.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001824; RecepttyrkinsII.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.

DR Pfam; PF00047; ig; 2.

DR ProDom; PD000001; Prot_kinase; 2.

DR SMART; SM00408; IGC2; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50835; IG LIKE; 3.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;

KW Phosphorylation; Receptor; Transferase; Transmembrane;

KW Tyrosine-protein kinase.

SQ SEQUENCE 1099 AA; 122934 MW; BCE126ACC116F740 CRC64;

Query Match 86.0%; Score 4957.5; DB 2; Length 1099;

Best Local Similarity 85.4%; Pred. No. 6.7e-290;

Matches 945; Conservative 75; Mismatches 78; Indels 9; Gaps 3;

QY 1 MRLPGAMPALALKCELLLSLLSLLLEPQISQGLVVTTPPGPELVLVNVSSTFVLTCSGSAPV 60

Db 1 MGLPGVIPALVLRGQ-LLSLVLLGPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPV 59

QY 61 VWERMSQBPPOEMAKAQDGTSSVLTLTNLTGLDTGEYFCTHDSRGLTDERKRLYIFV 120

Db 60 MWEQMSQVPWQEAAMNQDGTSSVLTLTNVTGGDTGEYFCVYNNNSLGPSELSEKRIYIFV 119

QY 121 PDPTVGFLPNDAAELFIFLTEITEITPCRVTDLPQLVVTLHEKKGDVALPVYDHQRGFS 180

Db 120 PDPTWDFLPMDSEDLFIFVTDVTEITPCRVTDLPQLEVTLHEKKVDIPLHVPYDHQRGFT 179

QY 181 GIFEDRSYICKTTIGDREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240

Db 180 GTFEDKTYICKTTIGDREVSDTYVYSLQVSSINVSNAVQTVVRQGESITIRCIVMGN 239

QY 241 DVNFEWTPRKESGRVPEVPTDPLLDMPYHIRSILHIPSAELEDSTYTCNVTESVNDH 300

Db 240 DVNFEQWTPRMKSGRLVEPVTDFLGVPSPRIGSILHIPTAEUSDSTYTCNVSVSNDH 299

QY 301 QDEKAINITVVEGCVYRLLGEVGTLOFAELHRSRTLOVVFAYDPPPTVWFKNRNLGDS 360

Db 300 GDEKAINISVIENGIVYRLLLETGLDVEIAELHRSRTLRVVFAYEMPSVLWLKDNRTLGD 359

QY 361 SAGETALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPRVL 420

Db 360 GAGELVLTSTRNMSETRYVSELTIVRVKVSEAGYTMRAFHEDEDEVQLSFKLQNVNPRVL 419

QY 421 ELSSEHPDSGEQTVRCRGRMPQPNIIWSACRDLK-RCPRELPPTLLGNSSEESQLETN 479

Db 420 ELSSEHPANGEQTIRCRGRGMPQPNVTWSTCRDLKSRCPKLSPTPLGNSSEESQLETN 479

QY 480 VTYWEEEQEFVWSTLRLOHQVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAIL 539

Db 480 VTFWEEDQEYEVVSTLRLRHVDPQLSVRCMLQNSMGGDSQEVTVVPHSLPFKVVVISAIL 539

QY 540 ALVVLTIIISLIILIMLWQKKPRYEIRWKVIESVSSDGDGHEYIYVDPQMLPYDSTWELPRDQ 599

Db 540 ALVVLTVISLIILIMLWQKKPRYEIRWKVIESVSSDGDGHEYIYVDPVQLPYDSTWELPRDQ 599

QY 600 LVLGRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSSELKIMSHLG 659

Db 600 LVLGRTLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSSELKIMSHLG 659

QY 660 PHLNVVNLIGACTKGGPIYIITEYCRYGDLVDYLHRNKHFTLQHHSDKRRPPSAELYSNA 719

Db 660 PHLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHFTLQRHSNKHCHPPSAELYSNA 719
Qy 720 LPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESNMYMAPYDNYV 779
Db 720 LPVGFSLPSHLNLTGESDGGYMDMSKDESIDYVPMLDMKGDIKYADIESPSYMAPYDNYV 779
Qy 780 PSAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKL 839
Db 780 PSAPERTYRATLINDSPVLSYTDLVGFSYQVANGMDFLASKNCVHRDLAARNVLICEGKL 839
Qy 840 VKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTL 899
Db 840 VKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTL 899
Qy 900 GGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFEIRPPESQLVLLLE 959
Db 900 GGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKWEEKFETRPPFSQLVLLLE 959
Qy 960 RLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSLDTSVLYTAVQPNESDN 1019
Db 960 RLLGEGYKKYQQVDEEFLRSDHPAILRSQARFPGIHSRLSPDTSVLYTAVQPNESDN 1019
Qy 1020 DYIIPDPKPVEADEGLEPSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLELQ 1079
Db 1020 DYIIPDPKPDVADEGLEPSPSLASSTLNEVNTSSTISCDSPLELQEEEPQ-----Q 1072
Qy 1080 VEPEPELEQLPDSGCCPAPRAEADSFL 1106
Db 1073 AEPEAQLEQPDSDGCGPLAEADSFL 1099

RESULT 6

P79749 PRELIMINARY; PRT; 1048 AA.
AC P79749;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor beta.
GN Name=PDGFRbeta;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129405; PubMed=8973913;
RA How G.F., Venkatesh B., Brenner S.;
RT "Conserved linkage between the puffer fish (Fugu rubripes) and human
RT genes for platelet-derived growth factor receptor and macrophage
RT colony-stimulating factor receptor."
RL Genome Res. 6:1185-1191(1996).
DR EMBL; U63926; AAC60062.1; -.
DR PIR; T30815; T30815.
DR HSSP; P35968; 1VR2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.

DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1048 AA; 117867 MW; 7363EFD38D9B13C CRC64;

Query Match 41.7%; Score 2403; DB 2; Length 1048;
Best Local Similarity 48.5%; Pred. No. 5.8e-136;
Matches 518; Conservative 159; Mismatches 321; Indels 70; Gaps 18;

Qy 9 ALALKGELLLLSL---LLLLPQISQGLVVTTPPGPELVNLVSSTFVLTCSGSAPVWVERM 65
Db 4 ASAMRAAVLHLTVLALALLSSCTTVSCLKIVPEEKQLLAEGSSLSLTGAGSSETWDLK 63
Qy 66 SQEPPQEMAKA-----QDGTFSVLTLTNLTGLDTGEYFCTHNDSRGLETDERK 115
Db 64 SDDVFFQMKAESSDLNKKIVQSNSTASVLTLLWHVDWKNATAVYQC-----REQLTGEIKE 118
Qy 116 LYIFVPD----PTVGFLPNDAAELFIFLFEIT-EITPCRVTDPOLVVTLLHEKKGDVALP 170
Db 119 VAVFVPDRFSPQTLRFI----ESSHGMVTKTSGESTVPCVVTNPNITVTLTKDLDLPVN 174
Qy 171 VPYDHRGFGSIFEDRSYIKTTIGDREVDSDAYVYVRLQV-SSINVSNAVQTVVROGE 229
Db 175 GYVVPSEGFKAYLDYRTYVCRGELNGEVKESQAFNVYSIHVPEDIDAYVNASQTVLKQGE 234
Qy 230 NITLMCIVIGNDVVNFETYPKESGRLVEPVTDFLLDMPYHIRSILHIPSAELEDSTY 289
Db 235 PLTVNCTVQGVELVLFSDIPNRD--IVKHKPETVVLVSATMRSCLVFPHPATVAHSGTY 291
Qy 290 TCNVTESVNDHQDEKAINITTVESGYVRLGGEVGTQLQFAELHRSRTLQVVFAYPPPTVL 349
Db 292 VCHAHSTQDKAFASVNITVLERGFVAVKSTRKQNTAELQENVELRVEIEAYPPQIR 351
Qy 350 WFXDNRTLGDSSAGEIALSTRNVSSETRVYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSF 409
Db 352 WKKD----GAPVRGDKTIIIRQEHHEIRYVITLTLVRVTEQKGLYALTINDDVKEVTF 407
Qy 410 QLQINVVRVLELSESHPSDGEQTVRCGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS 469
Db 408 ALEVQVLARIKDLTDHPLPGKQLVTCVAEGVPTPTIQWYSCDSMLKCNNQTSLSWQLKA 467
Qy 470 SEESQLETNVTYWEEQEFEV---VSTLRQLQHVDRPLSVRCTLRNAVGO-DTQEVIVVP 525
Db 468 DPELLSIHTSVT--EARQTNVRSQVTFFKPQHT---TVRCETTQEGLIIDFRDVKLVS 521
Qy 526 HSLPPKVVVISAILAVVLTIIISLIILIMLWQKPRYEIRWKVIESVSSDGEHYIYVDPM 585
Db 522 SSLSFQVLLAVLTLVPIIIMSIILIAVWKKKPRYEIRWKVIESVSQDGEHYIYVDPI 581
Qy 586 QLPYDSTWELPRDQLVLGRTLGSAGFQWVEATAHGLSHSQATMKVAVKMLKSTARSEK 645
Db 582 HLPYDLAWEMPRDNLVLGRTLGSAGFGRVVEATAHGLSHSQSIKAVKMLKATARRSET 641
Qy 646 QALMSELKIMSHLGPLHNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHRNKHFTLQHS 705
Db 642 QALMSELKIMSHLGPLHNVNLLAACTKHGPLYLVTEYCRYGDLVDYLHRNKHFTLQYVL 701
Qy 706 DKRRPPSAELYSNALPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765
Db 702 DKNQDGSLSISGGSTPLS-QRKGYSVFGSESDGGYMDMSKDEPAVYVPMQEQMDTIKYAD 760
Qy 766 IESSNYMAPY--DNYVPSAPERTCRATLINESPVLSDLVGFSYQVANGMEFLASKNCV 823
Db 761 IQSPSPYESPYQQDLYQEQQGGRV--DLVISDSPALTYDLLGFSYQVAKGMEFLASKNCV 818
Qy 824 HRDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTL 883
Db 819 HRDLAARNVLICEGKLVKICDFGLARDIMHDSNYISKGSTFLPLKWMAPESIFHNLYTTL 878

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=PDGFR-a;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302546; PubMed=10842055; DOI=10.1016/S0925-4773(00)00321-X;
RA Ataliohis P.;
RT "Platelet-derived growth factor A modulates limb chondrogenesis both
RT in vivo and in vitro.";
RL Mech. Dev. 94:13-24(2000).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-
CC 1/PDGF receptor subfamily.
DR EMBL; AF188842; AAF01460.1; -.
DR HSSP; P36888; 1RUB.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM0219; TyrcK; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1087 AA; 122939 MW; F3306BDD3D983E31 CRC64;

Query Match 39.4%; Score 2270; DB 2; Length 1087;
Best Local Similarity 44.1%; Pred. No. 6.4e-128;
Matches 499; Conservative 176; Mismatches 361; Indels 96; Gaps 21;

QY 12 LKGEALLLSLLLEPQISQGLVVTTPPGPELVNVSSSTFVLTCGSGAPVWERMMSQEPPO 71
DB 15 LTGPLLTLQCLPL-----PTIVPNRNMVYVQLNSNFTLKCSGDSVSW----QYPVT 62

QY 72 EMAKAQD-----GTFSSVLTLTNLTGLDTGEYFCTHNSRGLSTD-ERKRLYIFVDP 122
DB 63 EGSHRIDIRHEENNSGLFVTVLEVGNASAAHTGMVVCYNNHTQVEDGEVEGKDIIYIVDP 122

QY 123 PTVGFLPNDAAELFIFLITEITEITPCRVTDLPQVVTLHEKGDVALPVVDHQGFSGI 182
DB 123 PDMFPVPSLPEDQFILVEGDPPTVIPCRTSDPSAEVTLVNSL-DKPVYAFYDSKQGFVGN 181

QY 183 FEDRSYICKTTIGDREVDSDAYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIGND 241
DB 182 FLAGPYTCKTMVKGVEKSDFLIYLIRATSQLPVEIEALKTVYKTGETIVVTCVVDNE 241
QY 242 VVNFENTYPRKESGRVPEVPTDFLLDMP-YHIRSILHIPSAELEDSTGYTCNVTVESVNDH 300

DB 242 VVNLOWNYPGKVKEGLIKLDD--IKVPSQKLVYMLTIPDVLVKDTGDIYCTARHATKEV 299
QY 301 QDEKAINITVVEGCVRLIGVGTLOFAELHRSRTLQVFEAYPPPTVLWFKDNRTLGDS 360
DB 300 KENKKVITVHDKGFHLEPQFSPLEAVNLHEVKNFVVDVQAYPAPKMYLWLNKDVNTLIEN 359
QY 361 SAGEIALSTRNVSETRVSELTSLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVL 420
DB 360 LT-EIVTSSNRVQETRFQSVLKLIRAKEEDSGTILWLKNEDEIKRYTFSLLIQVPALIL 418
QY 421 ELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS-----S 470
DB 419 DLMDDHQSGAGRQTVRCCLAEGTPLPDVEWLVCDDIKKCSNDTSWTLLTNNISDIHMEHL 478
QY 471 EEESQLETNVTYWEEOEFVWSTLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPHSLPF 530
DB 479 DERNNVESQVTF-----QKVEETLAVRCVARNDLGAVTREKLKLVAPTLS 523
QY 531 KVVVISAILALVLTIIISLILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYD 590
DB 524 ELTVAAAVLVLLVIVIIISLIVLWQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYD 583
QY 591 STWELPRDQLVLGRTLGSGAFQVWEATAHGLSHSQATMKVAVKMLKSTARSSKQALMS 650
DB 584 SRWEFPRDGLVLGRILGSGAFKVGVEGTAYGLRSQPMKVAVKMLKPTARSSKQALMS 643
QY 651 ELKIMSHLGPHLNVNLLGACTKGGPYIITEYCRYGDLVDYLHRNKHTFLQHSDDKRRP 710
DB 644 ELKIMTHLGPHLNVNLLGACTKSGPIYIITEYCFYGDVLVNLHKNRDNFSLRHEPK--- 700
QY 711 PSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESDVDYVPMMLDMKGDVKYADIES 769
DB 701 PKKDLDFGMNPADESTRSYVILSFENTGEYMDMKQADTTQYVPMLEKKGSKYSDIORS 760
QY 770 NYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLA 828
DB 761 VYDRPASYYKKSLSESEVKNLLSDDGSEGLSLDLSFTYQVARGMEFLASKNCVHRDLA 820
QY 829 ARNVLTCEGLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMS 888
DB 821 ARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLVTTLSDVMS 880
QY 889 FGILLWEIFTLGGTPYPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEKFEIR 948
DB 881 YGILLWEIFSLGGILYPGMVVDSTFYNKIKSGYRMAKPDHATNEVEIYIMVKWNEPEKR 940
QY 949 PPFSQLVLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVL 1008
DB 941 PSFYHLSEIVESSLPGEYKKSVEKIHLDFLKSDDHPAVTR-----MRGDCDNAYIG 990
QY 1009 YT-----AVQPN-----GDNDYIIPDPKPEVADEGPLEGSPSLASSTLNEVNT 1054
DB 991 VTYKNEDKIKDRESGFDEQRLSADSGYITPLPDIDPVSEDE---LGKRNRRHSSQTSEESA 1047
QY 1055 SSTISCDSPLPEQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEADSFL 1106
DB 1048 IETGSSSTFIKRED-----ETIEDIMMDDIGIDSSDL-VEDSFL 1087

RESULT 15
Q9DE49
ID Q9DE49 PRELIMINARY; PRT; 1059 AA.
AC Q9DE49;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=pdgfra;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2005, 05:13:43 ; Search time 142.389 Seconds
(without alignments)
3916.424 Million cell updates/sec

Title: US-10-027-400-2
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMDDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5652	100.0	1089	1	PGDS_HUMAN	P16234 homo sapien
2	5400	95.5	1079	2	Q6E7G6	Q6e7g6 canis famil
3	5232	92.6	1089	2	Q7TSJ3	Q7tsj3 mus musculu
4	5229	92.5	1089	1	PGDS_MOUSE	P26618 mus musculu
5	5190.5	91.8	1088	1	PGDS_RAT	P20786 rattus norv
6	4577	81.0	1087	2	Q9PUF6	Q9puf6 gallus gall
7	4246	75.1	1087	1	PGDS_XENLA	P26619 xenopus lae
8	4228	74.8	1087	2	Q7ZY71	Q7zy71 xenopus lae
9	3715	65.7	743	2	Q6P4H5	Q6p4h5 homo sapien
10	3592	63.6	790	2	Q8C4N3	Q8c4n3 mus musculu
11	3419.5	60.5	1062	2	Q8AXC7	Q8axc7 fugu rubrip
12	3363	59.5	1059	2	Q9DE49	Q9de49 brachydanio
13	3296	58.3	1078	2	Q8AXC8	Q8axc8 fugu rubrip
14	2692	47.6	849	2	Q7Z608	Q7z608 homo sapien
15	2354.5	41.7	1106	1	PGDR_HUMAN	P09619 homo sapien
16	2336.5	41.3	1098	1	PGDR_MOUSE	P05622 mus musculu
17	2327	41.2	1099	2	Q7TMR8	Q7tmr8 mus musculu
18	2326	41.2	1097	1	PGDR_RAT	Q05030 rattus norv
19	2285.5	40.4	1103	2	Q6QNF3	Q6qnf3 canis famil
20	2182.5	38.6	1048	2	P79749	P79749 fugu rubrip
21	2132.5	37.7	686	2	Q75WK5	P75wk5 oryzias lat
22	2043	36.1	486	2	Q8CGH8	Q8cgh8 mus musculu
23	1914.5	33.9	457	2	Q90269	Q90269 brachydanio
24	1835.5	32.5	986	2	Q8UVR9	Q8uvr9 fugu rubrip
25	1554.5	27.5	976	2	Q9W755	Q9w755 brachydanio
26	1553.5	27.5	976	2	Q8JFR5	Q8jfr5 brachydanio
27	1527	27.0	984	2	Q8AXC6	Q8axc6 fugu rubrip
28	1489	26.3	978	1	KIT_CAPHI	Q28317 capra hircu
29	1481.5	26.2	977	1	KIT_BOVIN	P43481 bos taurus
30	1472	26.0	964	2	Q97744	Q97744 sus scrofa
31	1472	26.0	964	2	Q9TQQ0	Q9tqq0 sus scrofa

RESULT 1
PGDS_HUMAN
ID PGDS_HUMAN STANDARD; PRT; 1089 AA.
AC P16234; Q96KZ7;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE (PDGF-R-alpha) (CD140a antigen).
GN Name=PDGFRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89130149; PubMed=2536956;
RA Matsui T., Heidaran M., Miki T., Popescu N., la Rochelle W., Kraus M.,
RA Pierce J., Aaronson S.;
RT "Isolation of a novel receptor cDNA establishes the existence of two
RT PDGF receptor genes.";
RL Science 243:800-804(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89296915; PubMed=2544881;
RA Claesson-Welsh L., Eriksson A., Westermark B., Heldin C.H.;
RT "cDNA cloning and expression of the human A-type platelet-derived
RT growth factor (PDGF) receptor establishes structural similarity to the
RT B-type PDGF receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4917-4921(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=96163874; PubMed=8586421;
RA Kawagishi J., Ku T.;
RT "Structure, organization, and transcription units of the human alpha-
RT platelet-derived growth factor receptor gene, PDGFRA.";
RL Genomics 30:224-232(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

ALIGNMENTS

32	1470.5	26.0	975	2	Q7YRV7	Q7yrv7 canis famil
33	1469.5	26.0	979	2	Q8WN23	Q8wn23 canis famil
34	1469	26.0	964	2	Q9TQQ1	Q9tqq1 sus scrofa
35	1469	26.0	978	2	Q9XS93	Q9xs93 canis famil
36	1463.5	25.9	975	1	KIT_CANFA	Q97799 canis famil
37	1461.5	25.9	960	1	KIT_CHICK	Q08156 gallus gall
38	1460	25.8	974	2	Q63702	Q63702 rattus ratt
39	1458	25.8	978	2	Q63116	Q63116 rattus norv
40	1457.5	25.8	972	2	Q99662	Q99662 homo sapien
41	1454.5	25.7	976	1	KIT_HUMAN	P10721 homo sapien
42	1453.5	25.7	979	2	Q8C8K9	Q8c8k9 mus musculu
43	1452	25.7	972	2	Q761I0	Q761i0 callithrix
44	1450.5	25.7	975	2	Q6QJB8	Q6qjb8 mus musculu
45	1450.5	25.7	975	2	Q7TS86	Q7ts86 mus musculu

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP DISEASE.
RX MEDLINE=22547205; PubMed=12660384; DOI=10.1056/NEJMoa025217;
RA Cools J., DeAngelo D.J., Gotlib J., Stover E.H., Legare R.D.,
RA Cortes J., Kutok J., Clark J., Galinsky I., Griffin J.D., Cross N.C.,
RA Tefferi A., Malone J., Alam R., Schrier S.L., Schmid J., Rose M.,
RA Vandenbergh P., Verhoef G., Boogaerts M., Wlodarska I.,
RA Kantarjian H., Marynen P., Coutre S.E., Stone R., Gilliland D.G.;
RT "A tyrosine kinase created by fusion of the PDGFA and FIP1L1 genes as
RT a therapeutic target of imatinib in idiopathic hypereosinophilic
RT syndrome.";
RL N. Engl. J. Med. 348:1201-1214(2003).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1185-1189 IN COMPLEX WITH
RP SLC9A3R1 AND PDGFRB.
RX MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;
RA Karthikeyan S., Leung T., Ladias J.A.A.;
RT "Structural determinants of the Na+/H+ exchanger regulatory factor
RT interaction with the beta 2 adrenergic and platelet-derived growth
RT factor receptors.";
RL J. Biol. Chem. 277:18973-18978(2002).
CC -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a
CC tyrosine-protein kinase activity.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P16234-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P16234-2; Sequence=VSP 007833, VSP 007834;
CC Note=No experimental confirmation available;
CC -!- DISEASE: A fusion of PDGFA and FIP1L1 (FIP1L1-PDGFA), due to an
CC interstitial chromosomal deletion, is the cause of some cases of
CC hypereosinophilic syndrome (HES) [MIM:607685], a rare hematologic
CC disorder characterized by sustained overproduction of eosinophils
CC in the bone marrow, eosinophilia, tissue infiltration and organ
CC damage.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGFR
CC receptor subfamily.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; M21574; AAA96715.1; -;
CC EMBL; M22734; AAA60048.1; -;
CC EMBL; D50017; BAA08742.1; -;
CC EMBL; D50002; BAA08742.1; JOINED.
CC EMBL; D50003; BAA08742.1; JOINED.
CC EMBL; D50004; BAA08742.1; JOINED.
CC EMBL; D50005; BAA08742.1; JOINED.
CC EMBL; D50006; BAA08742.1; JOINED.
CC EMBL; D50007; BAA08742.1; JOINED.
CC EMBL; D50008; BAA08742.1; JOINED.
CC EMBL; D50009; BAA08742.1; JOINED.
CC EMBL; D50010; BAA08742.1; JOINED.
CC EMBL; D50011; BAA08742.1; JOINED.

DR EMBL; D50012; BAA08742.1; JOINED.
DR EMBL; D50013; BAA08742.1; JOINED.
DR EMBL; D50014; BAA08742.1; JOINED.
DR EMBL; D50015; BAA08742.1; JOINED.
DR EMBL; D50016; BAA08742.1; JOINED.
DR EMBL; BC015186; AAH15186.1; -;
DR PIR; A40162; PFHUGA.
DR PDB; 1GQ5; X-ray; -;
DR Genew; HGNC:8803; PDGFRA.
DR MIM; 173490; -;
DR MIM; 607685; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005018; F:platelet-derived growth factor alpha-recept. . .; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR 3D-structure; Alternative splicing; ATP-binding; Glycoprotein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 23 Alpha platelet-derived growth factor
FT CHAIN 24 1089 receptor.
FT DOMAIN 24 524 Extracellular (Potential).
FT TRANSMEM 525 549 Potential.
FT DOMAIN 550 1089 Cytoplasmic (Potential).
FT DOMAIN 24 113 Ig-like C2-type 1.
FT DOMAIN 202 306 Ig-like C2-type 3.
FT DOMAIN 319 410 Ig-like C2-type 4.
FT DOMAIN 593 954 Protein kinase.
FT DOMAIN 1041 1087 Ser-rich.
FT NP_BIND 599 607 ATP (By similarity).
FT BINDING 627 627 ATP (By similarity).
FT ACT_SITE 818 818 By similarity.
FT MOD_RES 849 849 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 76 76 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 103 103 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 179 179 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 359 359 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 458 458 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 468 468 N-linked (GlcNAc. . .) (Potential).
FT VARSPIC 210 218 ATSELDLEM -> GTCIISPLL (in isoform 2).
FT FTId=VSP_007833.
FT Missing (in isoform 2).
FT FTId=VSP_007834.
FT SEQUENCE 1089 AA; 122669 MW; 5E3FB9940ACD1BE8 CRC64;
SQ
Query Match 100.0%; Score 5652; DB 1; Length 1089;
Best Local Similarity 100.0%; Pred. No. 5.3e-297;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSWQYP 60
|||||

Db	1	MGTSHPAPFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSSFSLSRCFGESEVSWQYP	60
Qy	61	MSEESSDVIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY	120
Db	61	MSEESSDVIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY	120
Qy	121	VPDPVAFVPLGMTDYLIVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASYDSRQGFNG	180
Db	121	VPDPVAFVPLGMTDYLIVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASYDSRQGFNG	180
Qy	181	TFTVGPYICEATVKGKQFQIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICEATVKGKQFQIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWTPGVEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAAROATREVK	300
Db	241	EVVDLQWTPGVEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAAROATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIRISWLKNNLTLIENL	360
Qy	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Qy	421	VDDHSGTGGQTVRCTAEGTPLPDIEWMICDKIKCNETSWTILANNVSNIIITEIHSRD	480
Db	421	VDDHSGTGGQTVRCTAEGTPLPDIEWMICDKIKCNETSWTILANNVSNIIITEIHSRD	480
Qy	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540
Db	481	RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540
Qy	541	SLIVLVVWVKQPRYEIRWRVIESIPDGHEIYIYVDPMLPYDSRWEFPRDGLVLRVLG	600
Db	541	SLIVLVVWVKQPRYEIRWRVIESIPDGHEIYIYVDPMLPYDSRWEFPRDGLVLRVLG	600
Qy	601	SGAFKVVVEGTAYGLSRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660
Db	601	SGAFKVVVEGTAYGLSRSQPVVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLNIVNL	660
Qy	661	LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIIFGLNPADESTSY	720
Db	661	LGACTKSGPIYIIITEYCFYGDVNYLHKNRDSFLSHHPEKPKKELDIIFGLNPADESTSY	720
Qy	721	VILSPENNGDYMDKQADTTQVYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK	780
Db	721	VILSPENNGDYMDKQADTTQVYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK	780
Qy	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQKIVKICDFGLA	840
Db	781	LLSDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQKIVKICDFGLA	840
Qy	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTPYPGWM	900
Db	841	RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGGTPYPGWM	900
Qy	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKPSFYHLSEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDPVPEEEDLGKRNHSSQTSEESAIEGTSSSSTFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL 1089	
Db	1081	SDLVEDSFL 1089	

RESULT 2	
Q6E7G6	
ID	Q6E7G6 PRELIMINARY; PRT; 1079 AA.
AC	Q6E7G6;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Platelet-derived growth factor receptor alpha (Fragment).
GN	Name=PDGFRA;
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis;
OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Dickinson P.J., Roberts B.N., Mallen-StClair J., LeCouteur R.A.;
RT	"Evaluation of Receptor Tyrosine Kinase Expression in Canine Brain Tumors.";
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Mallen-StClair J., London C.A.;
RT	"The Role of PDGFRA in Canine Cancer.";
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-
CC	1/PDGF receptor subfamily.
DR	EMBL; AY525124; AAS91495.2; -.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR	GO; GO:0005468; P:protein amino acid phosphorylation; IEA.
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003598; Ig_c2.
DR	InterPro; IPR011009; Kinase like.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR001824; RecepttyrkinsIII.
DR	InterPro; IPR002290; Ser_thr_kinase.
DR	InterPro; IPR001245; Tyr_kinase.
DR	InterPro; IPR008266; Tyr_kinase_AS.
DR	InterPro; IPR009134; VEGFR.
DR	Pfam; PF00047; ig; 2.
DR	Pfam; PF00069; Pkinase; 1.
DR	PRINTS; PR01832; VEGFRECEPTOR.
DR	ProDom; PD000001; Prot_kinase; 2.
DR	SMART; SM00409; IG; 4.
DR	SMART; SM00408; IGC2; 3.
DR	SMART; SM00220; S_TKC; 1.
DR	SMART; SM00219; TyrKC; 1.
DR	PROSITE; PS50835; IG LIKE; 2.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW	Phosphorylation; Receptor; Transference; Transmembrane.
FT	NON TER 1
SQ	SEQUENCE 1079 AA; 121934 MW; 3DA424B9C1339D6B CRC64;

Query Match 95.5%; Score 5400; DB 2; Length 1079;
Best Local Similarity 95.9%; Pred. No. 2.2e-283;
Matches 1035; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

Qy	11	LGCLLTGLSLILCOLSLPILPNEKVKVQLNSSFSLSRCFGESEVSWQYPMSEESSDVE	70
Db	1	LGCLLAGPSLILCOLSLPILPNEKVKVQLNSSFSLSRCFGESEVSWHYPTSEENPNVE	60

RL Mol. Cell. Biol. 10:2237-2246(1990).

RN [2]

RX MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;

RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;

RT "Conservation in sequence and affinity of human and rodent PDGF ligands and receptors.";

RL Biochim. Biophys. Acta 1173:294-302(1993).

CC -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a tyrosine-protein kinase activity.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.

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DR EMBL; M63837; AAA40743.1; ALT_INIT.

DR EMBL; Z14118; CAA78488.1; --.

DR PIR; A34710; PFRPGA.

DR HSSP; P11362; 1FGK.

DR RGD; 3284; Pdgrfa.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001824; RecepttyrkinsIII.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.

DR InterPro; IPR009134; VEGFR.

DR Pfam; PF00047; Ig; 4.

DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR01832; VEGFRECEPTOR.

DR ProDom; PD000001; Prot_kinase; 2.

DR SMART; SM00409; IG; 3.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50835; IG LIKE; 3.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;

KW Tyrosine-protein kinase.

KW SIGNAL 1 23

FT CHAIN 24 1088 Alpha platelet-derived growth factor receptor.

FT DOMAIN 24 524 Extracellular (Potential).

FT TRANSMEM 525 548 Potential.

FT DOMAIN 549 1088 Cytoplasmic (Potential).

FT DOMAIN 25 112 Ig-like C2-type 1.

FT DOMAIN 213 305 Ig-like C2-type 3.

FT DOMAIN 318 409 Ig-like C2-type 4.

FT DOMAIN 592 953 Protein kinase.

FT NP_BIND 598 606 ATP (By similarity).

FT BINDING 626 626 ATP (By similarity).

FT ACT_SITE 817 817 By similarity.

FT MOD_RES 848 848 Phosphotyrosine (by autocatalysis) (By similarity).

FT CARBOHYD 41 41 O-linked (Potential).

FT CARBOHYD 75 75 N-linked (GlcNac. . .) (Potential).

FT CARBOHYD 102 102 N-linked (GlcNac. . .) (Potential).

FT CARBOHYD 178 178 N-linked (GlcNac. . .) (Potential).

FT CARBOHYD 352 352 N-linked (GlcNac. . .) (Potential).

FT	CARBOHYD	358	358	N-linked (GlcNac. . .) (Potential).
FT	CARBOHYD	457	457	N-linked (GlcNac. . .) (Potential).
FT	CARBOHYD	467	467	N-linked (GlcNac. . .) (Potential).
FT	CONFLICT	150	150	L -> R (in Ref. 2).
FT	CONFLICT	519	519	S -> T (in Ref. 2).
SQ	SEQUENCE	1088	AA; 122641	MW; 590C8BB0418801E7 CRC64;
Query Match 91.8%; Score 5190.5; DB 1; Length 1088;				
Best Local Similarity 90.9%; Pred. No. 4.8e-272;				
Matches 990; Conservative 55; Mismatches 43; Indels 1; Gaps 1;				
Qy	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENKVVQLNSSPSLRCFGESEVSWQYP	60	
Db	1	MGTSQ-AFLVLSCLLTGPSLIVCQLLLPSILPNENKIVPLSSPSLRCFGESEVSWQHP	59	
Qy	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYY	120	
Db	60	MSEEDPNVEIRTEENSSLFVTVLEVVNASAAHTGWYTCYNNHTQTEESEIEGRHIYY	119	
Qy	121	VPDPDAFVPLGMTDYLVIIVEDDSAIIPCRITDPETVTLHNSGVVPASYSRQGFNG	180	
Db	120	VPDPMAFVPLGMTDSLVIIVEDDSAIIPCLTDPDTEVTLHNNGRVLPASYSRQGFNG	179	
Qy	181	TFTVGPYICEATVGKKFQITPENVYALKATSELDEMEALKTVYKSGETIVVTCVAFNN	240	
Db	180	TFSVGPYICEATVRGRTFKTSFNVYALKATSELNLEMDTRQTVYKAGETIVVTCVAFNN	239	
Qy	241	EVVDLQWTPYGEVKGKITMLEIKVPSIKLVYTLTVPEATVKDGDYECARQATREVK	300	
Db	240	EVVDLQWTPYGEVRNKGITMLEIKLPSIKLVYTLTVPKATVKDGDYECARQATKEVK	299	
Qy	301	EMKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLIENL	360	
Db	300	EMKVTISVHEKGFVQIRPTFGHLETVNLHQVREFVVEVQAYPTPRISWLKNNLTLIENL	359	
Qy	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEADVKSITFELLTQVPSSILD	420	
Db	360	TEITTDVQRSQETRYQSKLLIRAKEEDSGHYTIIQNDDDMKSYTFELSTLVPASILEL	419	
Qy	421	VDDHGSTGGQTVRCTAEGTLPDIEWMICKDKKCNNTSWTILANNVSNIIITEIHSRD	480	
Db	420	VDDHSGSGGQTVRCTAEGTLPDIEWMICKDKKCNNTSWTILASNVSNIIITEFHQRG	479	
Qy	481	RSTVEGRVTFAKVEETIAVRCIAKNLLGAENRELKLVAPTLSRSELTVAALVLLVIVII	540	
Db	480	RSTVEGRVSFAKVEETIAVRCIAKNLDLGIGNRELKLVAPLSRSELTVAALVLLVIVIV	539	
Qy	541	SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPQMLPYDSRWEPFRDGLVLRVLG	600	
Db	540	SLIVLVVWVKQPRYEIRWRVIESISPDGHEYIYVDPQMLPYDSRWEPFRDGLVLRILG	599	
Qy	601	SGAFKVVVEGTAYGLSRSPQVKNVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNVNL	660	
Db	600	SGAFKVVVEGTAYGLSRSPQVKNVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNVNL	659	
Qy	661	LGACTKSGPIYIIITEYCFYGLVNLVYHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY	720	
Db	660	LGACTKSGPIYIIITEYCFYGLVNLVYHKNRDSFMSRHRPEKPKKDLIDIFGLNPADESTRSY	719	
Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMULDSEVKN	780	
Db	720	VILSFENNGDYVDMKQADTTQYVPMLEKVEYSKYSDIQRSLYDRPASYYKKSMULDSEAKN	779	
Qy	781	LLSDDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840	
Db	780	LLSDDDSEGLTLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	839	
Qy	841	RDIMHDSNVYVSKGSTFLPVKNWAPESIFDNLVYTTLSDVWVSGILLWEIFSLGGTYPGWM	900	
Db	840	RDIMHDSNVYVSKGSTFLPVKNWAPESIFDNLVYTTLSDVWVSGVLLWEIFSLGGTYPGWM	899	
Qy	901	VDSTFYNNKIKSGYRMAKPDHATSEVYEIMVKCNWSEPEKRPSPHYLSEIVENLLPGQYKK	960	

Db 900 VDSTFYNKIKSGYRMAKPDHATSEVVEIMVQCWNSEPEKRPSPFYHLSEIVENLLPGQYKK 959

Qy 961 SYEKIHLDFLKSDHPAVARMRVDSNDAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYII 1020

Db 960 SYEKIHLDFLKSDHPAVARMRVDSNDAYIGVTYKNEEDKLKEWEGGLDEQRLSADSGYII 1019

Qy 1021 PLPDDPVPPEEEDLGKRNHRSSQTSEESAIE TGSSSSSTFIKREDETIEDIMMDDIGIDS 1080

Db 1020 PLPDDPVPPEEEDLGKRNHRSSQTSEESAIE TGSSSSSTFIKREDETIEDIMMDDIGIDS 1079

Qy 1081 SDLVEDSFL 1089

Db 1080 SDLVEDSFL 1088

RESULT 6

Q9PUF6 PRELIMINARY; PRT; 1087 AA.

AC Q9PUF6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Platelet-derived growth factor receptor alpha.

GN Name=PDGFR-a;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RX MEDLINE=20302546; PubMed=10842055; DOI=10.1016/S0925-4773(00)00321-X;

RA Ataliotis P.;

RT "Platelet-derived growth factor A modulates limb chondrogenesis both in vivo and in vitro.";

RL Mech. Dev. 94:13-24(2000).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-1/PDGF receptor subfamily.

DR EMBL; AF188842; AAF01460.1; -.

DR HSSP; P36888; 1RJB.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001824; RecepttyrkinasII.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.

DR Pfam; PF00047; ig; 1.

DR PRINTS; PR01832; VEGFRECEPTOR.

DR ProDom; PD000001; Prot_kinase; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;

KW Phosphorylation; Receptor; Transmembrane;

KW Tyrosine-protein kinase.

SQ SEQUENCE 1087 AA; 122939 MW; F3306BDD3D983E31 CRC64;

Query Match 81.0%; Score 4577; DB 2; Length 1087;

Best Local Similarity 80.3%; Pred. No. 7.1e-239;

Matches 875; Conservative 95; Mismatches 116; Indels 4; Gaps 4;

Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNEKVKVQLNSSFSRLRCFGESEVSWQYP 60

Db 1 MGTPPRTFLILGCFLTGPLLTLCLPLPTIVPNRNMVVQLNSNFTLKCSGDSEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNSGLFVTVLVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

Db 61 VT-EGSHRIDIRHEENNSGLFVTVLVGNASAAHTMVVYCYNHTQVEDGEVEGKIYIY 119

Qy 121 VPDPDVAFVPLGMTDYLIVVEDDDSAIIPCRRTDPETPVTLHNS-EGVVPASYDSRQFN 179

Db 120 VPDPDMPFVPSLPEDQFILVEEGDPTVIPCRSTSDPSAEBVTLVNSLDKPYAFYDSKQGFV 179

Qy 180 GTFTVGPYICEATVKGKFKQTIPFNVIYALKATSELDEMEALKTVYKSGETIVVTCAVFN 239

Db 180 GNFLAGPYTCKTMVKGVEFKSDEFLIYLIRATSQLPVEIEALKTVYKTGETIVVTCVVD 239

Qy 240 NEWVDLQWTPGVEVKGGITMLEEIKVPSIKLVYTLTVPEATVKOSGDYECARQATREV 299

Db 240 NEVVNLQWNPYGVKEKGLIKLDDIKVPSQKLVYMLTIPDVLVKDTDYECTARHATKEV 299

Qy 300 KEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIEN 359

Db 300 KENKKVVI TVHDKGFIHLEPQFSPL EAVNLHEVKNFVVDVQAYPAPKMYWLKDNVTLIEN 359

Qy 360 LTEITTDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNE DAVKSYTFELLTQVPSSILD 419

Db 360 LTEIVTSSNRVQETRFQSVLKLIRAKEEDSGTILWLKNEDEIKRYTFSLLIQVPALILD 419

Qy 420 LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSR 479

Db 420 LMDDHQGSAGRTVRCCLAEGTPLPDVEWLVCCKDIKKCSNDTSWTLTNNISDIHMAHLD 479

Qy 480 DRSTVEGRVTFAKVEETI AVRCLAKNLLGAENRELKLVAPT LRSELTVAAA VLLVIVI 539

Db 480 ERNMVESQVTFQKVEETLAVRCVARNDLGAVTRELKLVAPT LRSELTVAAA VLLVIVI 539

Qy 540 ISLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDMQ LPYDSRWEFPRDGLVLRVL 599

Db 540 ISLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDMQ LPYDSRWEFPRDGLVLRIL 599

Qy 600 GSGAFGKVEGTAYGLSRSPVMKVAVKMLKPTARSSKQALMSELKIMTHLGPHLNIYN 659

Db 600 GSGAFGKVEGTAYGLSRSPVMKVAVKMLKPTARSSKQALMSELKIMTHLGPHLNIYN 659

Qy 660 LLGACTKSGPIYIITEYCFYGD LVNLYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719

Db 660 LLGACTKSGPIYIITEYCFYGD LVNLYLHKNRDNFLSRHPEKPKKDLDFGMNPADESTRS 719

Qy 720 YVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS DIQRSLYDRPAS YKKKSLDSEVK 779

Db 720 YVILSFENTGEYMDMKQADTTQYVPMLERKEGSKYS DIQRSVYDRPAS YKKKSLSESEVK 779

Qy 780 NLLSDDNSEGLTLDDLSTFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGL 839

Db 780 NLLSDDGSEGLSLDLLSTFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGL 839

Qy 840 ARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS DVMYSYGILLWEIFSLGGTYPGGM 899

Db 840 ARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS DVMYSYGILLWEIFSLGGILYPGM 899

Qy 900 MVDSTFYNKIKSGYRMAKPDHATSEVVEIYIMVKCWNSEPEKRPSPFYHLSEIVENLLPGQYK 959

Db 900 MVDSTFYNKIKSGYRMAKPDHATNEVVEIYIMVKCWNNEPEKRPSPFYHLSEIVESLLPGEYK 959

Qy 960 KSYEKIHLDFLKSDHPAVARMRVDSNDAYIGVTYKNEEDKLKDWEGLDEQRLSADSGYI 1019

Db 960 KSYEKIHLDFLKSDHPAVTRMGDCDNAYIGVTYKN-EDKIKDRESGFDEQRLSADSGYI 1018

Qy 1020 IPLPDIDPVPEEEDLGKRNHRSSQTSEESAIE TGSSSSSTFIKREDETIEDIMMDDIGID 1079

QY	664	CTKSGPIYITEYCFYGDLVNLYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVIL	723
Db	666	CTKSGPIYITEYCFYGDLVNLYLHKNRDNFQSRHPEKPKKDLDFGLNPADESTRSYVIL	725
QY	724	SFENNGYNDMKQADTTQYVPMLEKEVSKYSYDIQRSYDRPASYYKKSMLDSEVKNLLS	783
Db	726	SFENNGYNDMKQADTMQYVPMLEKPEPSKYSYDIQRSYDRPASYYKKKPL--SEVKNILS	783
QY	784	DDNSEGLTLDDLSSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDI	843
Db	784	DDGFEGLTVLDDLSTYQVARGMEFLASKNCVHRDLAARNVLLAAGKIVKICDFGLARDI	843
QY	844	MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTYPYGMVDS	903
Db	844	MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSFGILLWEIFSLGGTYPYGMIVDS	903
QY	904	TFYNKIKSGYRMAKPDHATSEVYEIMVKWNSEPEKRPSEFYHLSEIVENLLPGQYKKSYE	963
Db	904	TFYNKIKSGYRMAKPDHATHEVYDVMKWNSEPEKRPSEFRHSDIVESLLPMEYKRCYE	963
QY	964	KIHLDFLKSHPAVARMRVDSNAYIGVYTKNEEDKLKDWEGLDQRLSADSGYIIPLP	1023
Db	964	TVLHDFLKSHPAVATMRSDSDSNYIGVYTKNEH-KMKDRESGDFEQRLSADSGYIIPLP	1022
QY	1024	DIDPVEEDLGKRNHRSSQTSESAIETGSSSSTFIKREDETIEDIMDDDIGIDSSDL	1083
Db	1023	DIDPVEDES-GKRNHRSSQTSESAIETGSSSSTFIKRDEDETIEDIMDDDIGIDSSDL	1081
QY	1084	VEDSFL	1089
Db	1082	VEDSFL	1087

RESULT 8

Q7ZY71	PRELIMINARY;	PRT;	1087	AA.
ID	Q7ZY71			
AC	Q7ZY71;			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Pdgfra-prov protein.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RC	TISSUE=Embryo;				
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;				
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,				
RA	Richardson P.;				
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus				
RT	initiative."				
RL	Dev. Dyn. 225:384-391 (2002).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Embryo;				
RA	Klein S., Strausberg R.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).				
CC	-!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-				
CC	1/PDGF receptor subfamily.				
DR	EMBL; BC043948; AAH43948.1; -.				
DR	HSSP; P36888; 1RJB.				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0005524; F:ATP binding; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0016740; F:transferase activity; IEA.				
DR	GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.				
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.				
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.				
DR	InterPro; IPR003599; IG.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR011009; Kinase like.				
DR	InterPro; IPR000719; Prot_kinase.				
DR	InterPro; IPR001824; RecepttyrkinsIII.				
DR	InterPro; IPR001245; Tyr_pkinase.				
DR	InterPro; IPR008266; Tyr_pkinase_AS.				
DR	InterPro; IPR009134; VEGFR.				
DR	Pfam; PF00047; ig; 2.				
DR	PRINTS; PR01832; VEGFRECEPTOR.				
DR	ProDom; PD000001; Prot_kinase; 2.				
DR	SMART; SM00409; IG; 3.				
DR	SMART; SM00219; TyrKc; 1.				
DR	PROSITE; PS00835; IG LIKE; 3.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.				
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.				
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;				
KW	Phosphorylation; Receptor; Transferase; Transmembrane;				
KW	Tyrosine-protein kinase.				
SQ	SEQUENCE 1087 AA; 122585 MW; 2C094A5FB7C43566 CRC64;				

Query Match 74.8%; Score 4228; DB 2; Length 1087;

Best Local Similarity 75.2%; Pred. No. 5.3e-220;

Matches 817; Conservative 105; Mismatches 156; Indels 8; Gaps 6;

QY	7	AFLVLGCLL-TGLSLILCOLSLPSILPNENKVVQLNSSFSILRCFGESEVSWQYPMSEEE	65
Db	7	ASLILGCLLIIGPWAILAENPLPTIFPDKDELVQALHSSFTLKCTGESEVSWQNPSNPE	66
QY	66	SSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYVNHQTQTEENELEGRHIYIYVDPD	125
Db	67	KQNVVIRSEENNSGLFVSLILEVSDASAFDTGLYTCYVNHQTQTEESEIEGTDIYIYVDPN	126
QY	126	VAFVPLGMTDYLIVIVEDDDSAIIPCRITDTPETPTVLHNSG--VVPASYDSRQGFNGTFT	183
Db	127	VFPAPPGLFDHIIIVVEDESALVPCRTTDPSSSEVMLKNIESSRVTFVAFYDSKQGFAGNFP	186
QY	184	VGPYICEATVKGKFKQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVV	243
Db	187	PGSYICETTSNKMVYQTEPYILQTWKATHNISVEMEAPKTMFRAGETIAIDCIVLDNEVV	246
QY	244	DLQWYTPGEVKGKITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVKEMK	303
Db	247	DLKWYTPGKQGVGIRNVEESKVPYQRLVYTLTLANATTDSGEYECAVIHATLDNRVVK	306

Db 121 VPDPAVFPVPLGMDTYLVIVEDDSAIIPCRITDPETPTVLHNSGVWPASYSRQGFNG 180
Qy 181 TFTVGPYICEATVKGKKFQIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240
Db 181 TFTVGPYICEATVKGKKFQIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVAVNN 240
Qy 241 EVVDLQWYTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Db 241 EVVDLQWYTPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVVEVRAYPPTPRISWLKNNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVVEVRAYPPTPRISWLKNNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTTIVAQNEDAVKSYTFELLTQVPSSILD 420
Qy 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Db 421 VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIITEIHSRD 480
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTIRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEIYIYVDPMQLPYDSRWEFPRDGLVLRVLG 600
Qy 601 SGAFGKVVVEGTAYGLRSQPMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPHLNIVNL 660
Db 601 SGAFGKVVVEGTAYGLRSQPMKVAVKMLKPTARSSSEKQALMSELKIMTHLGPHLNIVNL 660
Qy 661 LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719
Db 661 LGACTKSGPIYIITEYCFYGDVLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719

RESULT 10
Q8C4N3 PRELIMINARY; PRT; 790 AA.
AC Q8C4N3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30063B01 product:platelet derived growth factor receptor, alpha polypeptide, full insert sequence.
DE Name=pdgfra;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK081664; BAC38283.1; -.
DR HSSP; P36888; 1RJB.
DR MGD; MGI:97530; Pdgrfra.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0030539; P:male genital morphogenesis; IMP.
DR GO; GO:0009887; P:organogenesis; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 2.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; prot_kinase; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Receptor.
SQ SEQUENCE 790 AA; 88629 MW; FE13756876B68B95 CRC64;

Query Match 63.6%; Score 3592; DB 2; Length 790;
Best Local Similarity 88.8%; Pred. No. 8.4e-186;
Matches 687; Conservative 46; Mismatches 41; Indels 0; Gaps 0;
Qy 1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENKVVQLNSSFSLRCFGESEVSNQYP 60
Db 1 MGTSHQVFLVLSCLLTGGLISCLQLLLPSILPNENKIVQLNSSFSLRCVGESEVSNQHP 60

QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTREENELGRHIYY	120
Dd	61	: : : : : : : :	120
QY	121	VPPDPVAFVPLGMDTYLVIVEDDDSAIIPCRITDPETPVTLHNSEGVPASYDSRQGFNG	180
Dd	121	: : : : : : : :	180
QY	181	TFTVGPIYICEATVKKKFQTI PFNVYALKATSELDEMEALKT VYKSGETIVVTCAVFNN	240
Dd	181	: : : : : : : :	240
QY	241	EVDLQWTPYGEVKGKITMLEEIKVPSIKLVYTLTVP EATVKDSGDYECAARQATREVK	300
Dd	241	: : : : : : : :	300
QY	301	EMKVTVISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRI SWLKNNLTLIENL	360
Dd	301	: : : : : : : :	360
QY	361	TEITTDVEKIQEI RYSKLK LIRAKEEDSGHYTIVAQN ED AVKSYTFELLTQVPSSILD L	420
Dd	361	: : : : : : : :	420
QY	421	VDDHGSTGGQTVRCTAEGTPLPDIEWMICKDI KKNNETSWTILANNYSNIITEIHSRD	480
Dd	421	: : : : : : : :	480
QY	481	RSTVEGRVTFAKVEETIA VRCLAKNLLGAENRELKLVAPT LRSELTVA AAVLVLLVIVII	540
Dd	481	: : : : : : : :	540
QY	541	SLIVLVWIWKQPRY EIRWRVIESIPDGHEYI YVDPMQLPYDSRWEFRDGLVLGRVLG	600
Dd	541	: : : : : : : :	600
QY	601	SGAFKWVEGTAYGLSRQPVMKVAVKM LKPTARSSEKQALMSELKIMTHLGPHLNIVNL	660
Dd	601	: : : : : : : :	660
QY	661	LGACTKSGPIYIIITEYCFY GDLVNYLHKNRDSFLSHHP EKPKKELDIFGLNPADESTRSY	720
Dd	661	: : : : : : : :	720
QY	721	VILSFENN GDYMDMKQADTTQYVPEMLERKEVSKYS DIQRSLYDRPASVKKKSML	774
Dd	721	: : : : : : : :	774

```

RESULT 11
QBAXC7
ID QBAXC7 PRELIMINARY; PRT; 1062 AA.
AC QBAXC7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PDGFRalpha isoform 1.
GN Name=PDGFRalpha;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22481137; PubMed=12592706;
RA Williams H., Brenner S., Venkatesh B.;
RT "Characterization of the platelet-derived growth factor receptor alpha
RT and c-kit genes in the pufferfish Fugu rubripes.";
RL DNA Seq. 13:263-270(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

```

CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-
CC 1/PDGF receptor subfamily.
DR EMBL; AF456419; AAN87554.1; -.
DR HSSP; P36888; 1RJB.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0005021; F: vascular endothelial growth factor receptor. . ; IEA.
DR GO: GO:0006468; P: protein amino acid phosphorylation; IEA.
DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1062 AA; 118636 MW; 5439854FE174B832 CRC64;

-!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-

QY 563 ESISPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVILGSGAFGKVVEGTAYGLSRSQPV 622
||:|||||
Db 539 ESVSPDGHEYIYVDPMLPYDSRWEPFRDLVLRILGSGAFGKVVEGTAYGLSRSQPV 598
||:|||||
QY 623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNLLGACTKSGPIYIITEYCFY 682
|||||
Db 599 KVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNLLGACTKSGPIYIITEYCFY 658
|||||
QY 683 VNYLHKNRDSFLSHHPEKP-KKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQ 741
|||||:|||||
Db 659 VNYLHKNRDSFLNPKPEKSNKKELDIFGINPADESSRYVILSFESKGDYMDMKQADNTQ 718
|||||:|||||
QY 742 YVPMLEKEVSKYSDIQRLSYDRPASYYKKSMLDSEVKNLLSDDNSEGLTLDLLSFTYQ 801
|||||:|||||:|||||
Db 719 YVPMLEISNASKYSDLQGSNYDHPSPQKGSN--DGEMDQLLSDNMSEGLTTNDLLSFTYQ 776
|||||:|||||:|||||
QY 802 VARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKW 861
||:|||||
Db 777 VAKGMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPVKW 836
|||||
QY 862 MAPESIFDNLYTTLSDVWSYGILLWEIFSLGCTPYPGVMVDSTFYNKIKSGYRMAKDDHA 921
|||||:|||||:|||||:|||||
Db 837 MAPESIFDNLYTTLSDVWSYGILLWEIFSLGCTPYPGMIVDSSFYNKIKSGYRMSKEPHA 896
|||||:|||||:|||||:|||||
QY 922 TSEVYEIMVKCNSEPEKRPFSFVHLSSEIVENLLPGQYKKSYEKIHLDFLKSDDHPAVARNR 981
:|||||:|||||:|||||:|||||:|||||
Db 897 PQDYVDMMMKCNSEPEKRPSTFLGSLDSTIASLLPSSYKRHYERNVHFEFLKSDHPAVTRVC 956
|||||:|||||:|||||:|||||:|||||
QY 982 VDSNAYIGVTYKNEEDKLKWEGGLDEQRLSADSGYIIPLPDIDPVPPEEDLGKRNHRS 1041
||:|||||:|||||:|||||:|||||:|||||
Db 957 VDNDAYIGITYKN-QGKLKDRSGFDEQRLSSDSGYIIPLPDLDPISDEE-YGKRNHRS 1014
|||||:|||||:|||||:|||||:|||||
QY 1042 SQTSESAIETGSSSSSTFIKREDETIEDIDMDDDIGIDSSDLVEDSFL 1089
|||||:|||||:|||||:|||||:|||||
Db 1015 SQTSESAIETGSSSSSTFAKREGTLEDTITLDEMCLDCSLVEDSFL 1062
|||||:|||||:|||||:|||||:|||||

RESULT 12
Q9DE49
ID Q9DE49 PRELIMINARY; PRT; 1059 AA.
AC Q9DE49;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=pdgfra;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu L., Balasubramanian N.V., Ge R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-1/PDGF receptor subfamily.
CC EMBL; AF200951; AAG43479.1; -.
DR HSSP; P36888; 1RJB.
DR ZFIN; ZDB-GENE-990415-208; pdgfra.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1059 AA; 118210 MW; 0AE93E2ABD9A72F3 CRC64;

Query Match 59.5%; Score 3363; DB 2; Length 1059;
Best Local Similarity 61.5%; Pred. No. 3e-173;
Matches 659; Conservative 157; Mismatches 223; Indels 32; Gaps 14;

QY 28 PSILPNENEKVVQLNSSFSILRCFGESEVSWQYPM-SEBSSDVEIRNEENNSGLFVTVLE 86
||:|||||
Db 12 PLIWPQRESMEVSLHSTFRLTCRGQTELSWNGPVFIDDQTSVK-----KGLFISIVT 64
||:|||||
QY 87 VSSASAAHTGLTYCY---YNHQTTEENELEGRHIYIYVDPDPAFVPLGMDTY-LVIVED 142
||:|||||
Db 65 ISNATAVHTGEYVCSSEPEPSTEST-----IYIYVDPDQTPFVP-SMTPFENHVLTS 115
||:|||||
QY 143 DDSAIIIPCRRTTDPETPVTL--HNSEGVVPASYDSRQGFNGTFTVGPYICEATVKGKKQT 200
||:|||||
Db 116 YDEMEIPCRVTDPSASVSLIHMGTDQVMPSAYDSKRGFGLFGAGTYVCRALIHQNHS 175
||:|||||
QY 201 IPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITM 260
||:|||||
Db 176 IEYIVHGTGSDLRVELRAVKRTLTVGETITVDCVAKGSEVLEHDHWKYPGKLANRGPKT 235
||:|||||
QY 261 LEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVKEMKVTISVHEKGFIEIKPT 320
||:|||||
Db 236 VKENKL-NLEIYYTLTVTNASPKDSGIYACSIIDIMSNESQTKELTITVDHEFVHINPL 294
||:|||||
QY 321 FSQLEAVNLHEVKHFVVEVRAYPPIPRISWLKNLTLIENLTETDVEKIQEIRYSKLK 380
||:|||||
Db 295 IGPVETARLDEVPEFKVDIESFPAPKVTLWKDSSVLGDDTAETISLTLKIGETSYQGVLN 354
||:|||||
QY 381 LIRAKEEDSGHYTIVAQNEDAVKSYTFPELLTQVPSSILDVDDHHGSTGGQTVRCCTAEGT 440
||:|||||
Db 355 LIRAKAEDSGNYTVKAEIGSISTSYSFYLQVKVPPVIVDLIDVHHGSAAGQEVVCTAGGS 414
||:|||||
QY 441 PLPDIEWMICKOIKKCNNETS-WTILANNVSNIIITEIHSRDRSTVEGRVTFAKVEETIAV 499
||:|||||
Db 415 PFPEVDWDICKNLKHCANDSSQWMLPINSTDITVELQMVNDNHIESHIIFFHLEGTVAV 474
||:|||||
QY 500 RCLAKNLLGAENRELKLVAPTILRSELTVAAAVALLVIIISLIVLVVIWKQKPRYEIRW 559
||:|||||
Db 475 RCLARNDMGVWSREVKLMSSGPHSELTVAAAVALLVIIISLIVLVVIWKQKPRYEIRW 534
||:|||||
QY 560 RVIESISPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVILGSGAFGKVVEGTAYGLSRSQ 619
||:|||||
Db 535 RVIESVSPDGHEYIYVDPMLPYDSRWEPFRDGLVLRVILGSGAFGKVVEGTAYGLSRSQ 594
||:|||||
QY 620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNLLGACTKSGPIYIITEYCFY 679
||:|||||
Db 595 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHLNIVNLLGACTKSGPIYIITEYCFY 654
||:|||||
QY 680 GDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADT 739
||:|||||
Db 655 GDLVNYLHKNRDGFSLRHTTEKGGKDLDFGINPADESSRSYVILSLEKGDYMDMKQADT 714
||:|||||
QY 740 TQYVPMLEKKEVSKYSDIQRLSYDRPASYYKKSMLDSEVKNLLSDDNSEGLTLDLLSFT 799
||:|||||

Db 882 LGGTPYPGMIVDSSFYNKIKSGYRMSKPEHAPQDVYDMMKOWNSEPEKRPSTFLGLSDTI 941

QY 951 ENLLPGQYKKSYEKIHLDFLKSHPAVARMRVSDNAYIGVTYKNEEDKLKOWEGLDEQ 1010

Db 942 ASLLPSSYKRHYRVNHEFLKSDHPAVTRVCVNDNDAYIGITYKN-QGKLKORESGFDEQ 1000

QY 1011 RLSADSGYIIPLDIDPVPPEEEDLGKRNHSSQTSEESALETGSSSSTFIKREDETIEDI 1070

Db 1001 RLSSDSGYIIPLDLPISDEE-YGKRNHRHSSQTSEESALETGSSSSTFAKREGTELEDI 1059

QY 1071 DMDDIGIDSSDLVEDSFL 1089

Db 1060 TLDDDEMCLDCSDLVEDSFL 1078

RESULT 14

Q7Z608 PRELIMINARY; PRT; 849 AA.

AC Q7Z608;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE FIP1L1/PDGFR fusion protein.

GN Name=FIP1L1/PDGFR fusion;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=12808148; DOI=10.1073/pnas.0932698100;

RA Griffin J.H., Leung J., Bruner R.J., Caligiuri M.A., Briesewitz R.;

RT "Discovery of a fusion kinase in EOL-1 cells and idiopathic

RT hypereosinophilic syndrome.";

RL proc. Natl. Acad. Sci. U.S.A. 100:7830-7835(2003).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-

CC 1/PDGF receptor subfamily.

DR EMBL; AY229892; AAP69563.1; -.

DR HSSP; P36888; IRJB.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.

DR InterPro; IPR007854; Fip1.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001824; RecepttyrkinsIII.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.

DR Pfam; PF05182; Fip1; 1.

DR ProDom; PD000001; Prot_kinase; 2.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;

KW Phosphorylation; Receptor; Transferase; Transmembrane;

KW Tyrosine-protein kinase.

SQ SEQUENCE 849 AA; 94703 MW; 597527ED06A129FF CRC64;

Query Match 47.6%; Score 2692; DB 2; Length 849;

Best Local Similarity 74.6%; Pred. No. 4.3e-137;

Matches 551; Conservative 28; Mismatches 61; Indels 99; Gaps 12;

QY 352 NNLTLIENLITEITDVEKIQEIRYSKLIKIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411

Db 209 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRGTGN----SEKETALPSTKAE-FT 258

QY 412 QVPSSILDVDDHHGSTGGQTVRCTAEGTPLPDIEMMICKDIKKCNNET-SWTILANNVS 470

Db 259 SPSPFLKFTGLPPSRNSTSSQSTSTAS-----RKANSSVGKW----- 295

QY 471 NIITEIHSRDRSTVEGRVTFAKVVEETIAVRCLAKNLLGAENRELKLVAPTLLRSELTVAAA 530

Db 296 -----QDR-----YGRAE-----SPDLR---RLPGA 313

QY 531 VLVLVIVIIISLIVLVIMWKPRYEIRWRVIESISPDGHEVIYVDPMQLPYDSRWFEPR 590

Db 314 IDVIGQTITIS-----RVEGRRRANENS-----IQLPYDSRWFEPR 350

QY 591 DGLVLRVLSGSAFGKVVVEGTAYGLSRSQPMKVAVKMLKPTARSSKQALMSELKIMTH 650

Db 351 DGLVLRVLSGSAFGKVVVEGTAYGLSRSQPMKVAVKMLKPTARSSKQALMSELKIMTH 410

QY 651 LGPHLNIIVNLLGACTKSGPIYIITEYCFYGDLVNLYLHKNRDSFLSHHPEKPKKELDIFGL 710

Db 411 LGPHLNIIVNLLGACTKSGPIYIITEYCFYGDLVNLYLHKNRDSFLSHHPEKPKKELDIFGL 470

QY 711 NPADESTRSYVILSFENNGYMDMKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYYK 770

Db 471 NPADESTRSYVILSFENNGYMDMKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYYK 530

QY 771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830

Db 531 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 590

QY 831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFS 890

Db 591 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFS 650

QY 891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSTFYHLSEIV 950

Db 651 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSTFYHLSEIV 710

QY 951 ENLLPGQYKKSYEKIHLDFLKSHPAVARMRVSDNAYIGVTYKNEEDKLKOWEGLDEQ 1010

Db 711 ENLLPGQYKKSYEKIHLDFLKSHPAVARMRVSDNAYIGVTYKNEEDKLKOWEGLDEQ 770

QY 1011 RLSADSGYIIPLDIDPVPPEEEDLGKRNHSSQTSEESALETGSSSSTFIKREDETIEDI 1070

Db 771 RLSADSGYIIPLDIDPVPPEEEDLGKRNHSSQTSEESALETGSSSSTFIKREDETIEDI 830

QY 1071 DMDDIGIDSSDLVEDSFL 1089

Db 831 DMDDIGIDSSDLVEDSFL 849

RESULT 15

PGDR_HUMAN

ID PGDR_HUMAN STANDARD; PRT; 1106 AA.

AC P09619; Q8NSL4;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)

GN (PDGF-R-beta) (CD140b antigen).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88217915; PubMed=2835772;

RA Gronwald R.G.K., Grant F.J., Haldeman B.A., Hart C.E., O'Hara P.J.,

RA Hagen F.S., Ross R., Bowen-Pope D.F., Murray M.J.;

RT "Cloning and expression of a cDNA coding for the human platelet-

RT derived growth factor receptor: evidence for more than one receptor

RT class.";

RL proc. Natl. Acad. Sci. U.S.A. 85:3435-3439(1988).

RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=89096941; PubMed=2850496;
RA Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,
RA Oestman A., Betsholtz C., Heldin C.-H.;
RT "cDNA cloning and expression of a human platelet-derived growth factor
RT (PDGF) receptor specific for B-chain-containing PDGF molecules.";
RL Mol. Cell. Biol. 8:3476-3486(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 548-569 FROM N.A.
RX MEDLINE=97429921; PubMed=9285559; DOI=10.1038/sj.onc.1201267;
RA Chi K.D., McPhee R.A., Wagner A.S., Dietz J.J., Pantazis P.,
RA Goustin A.S.;
RT "Integration of proviral DNA into the PDGF beta-receptor gene in HTLV-
RT I-infected T-cells results in a novel tyrosine kinase product with
RT transforming activity.";
RL Oncogene 15:1051-1057(1997).
RN [5]
RP SEQUENCE OF 1046-1106 FROM N.A.
RX MEDLINE=89028677; PubMed=2846185; DOI=10.1016/0092-8674(88)90224-3;
RA Roberts W.M., Look A.T., Roussel M.F., Sherr C.J.;
RT "Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor
RT genes.";
RL Cell 55:655-661(1988).
RN [6]
RP SEQUENCE OF 33-47.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [7]
RP AUTOPHOSPHORYLATION SITES.
RX MEDLINE=89376563; PubMed=2550144; DOI=10.1016/0092-8674(89)90510-2;
RA Kazlauskas A., Cooper J.A.;
RT "Autophosphorylation of the PDGF receptor in the kinase insert region
RT regulates interactions with cell proteins.";
RL Cell 58:1121-1133(1989).
RN [8]
RP INTERACTION WITH APS.
RX MEDLINE=99142932; PubMed=9989826; DOI=10.1038/sj.onc.1202326;
RA Yokouchi M., Wakioka T., Sakamoto H., Yasukawa H., Ohtsuka S.,
RA Sasaki A., Ohtsubo M., Valius M., Inoue A., Komiya S., Yoshimura A.;
RT "APS, an adaptor protein containing PH and SH2 domains, is associated
RT with the PDGF receptor and c-Cbl and inhibits PDGF-induced
RT mitogenesis.";
RL Oncogene 18:759-767(1999).
RN [9]
RP CHROMOSOMAL TRANSLOCATION WITH TRIP11.
RX MEDLINE=98043615; PubMed=9373237;

RA Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;
RT "Fusion of the platelet-derived growth factor receptor beta to a novel
RT gene CEV14 in acute myelogenous leukemia after clonal evolution.";
RL Blood 90:4271-4277(1997).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.79 ANGSTROMS) OF 751-755 IN COMPLEX WITH
RP PIK3R1, AND COMPARISON WITH NMR ANALYSIS.
RX MEDLINE=21450159; PubMed=11567151; DOI=10.1107/S0907444901012434;
RA Paupit R.A., Dennis C.A., Derbyshire D.J., Breeze A.L., Weston S.A.,
RA Rowsell S., Murshudov G.N.;
RT "NMR trial models: experiences with the colicin immunity protein Im7
RT and the p85alpha C-terminal SH2-peptide complex.";
RL Acta Crystallogr. D 57:1397-1404(2001).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1102-1106 IN COMPLEX WITH
RP SLC9A3R1 AND PDGFRA.
RX MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;
RA Karthikeyan S., Leung T., Ladias J.A.A.;
RT "Structural determinants of the Na+/H+ exchanger regulatory factor
RT interaction with the beta 2 adrenergic and platelet-derived growth
RT factor receptors.";
RL J. Biol. Chem. 277:18973-18978(2002).
CC -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
CC tyrosine-protein kinase activity. Phosphorylates Tyr residues at
CC the C-terminus of PTPN11 creating a binding site for the SH2
CC domain of GRB2.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with
CC APS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DISEASE: Involved in a form of chronic myelomonocytic leukemia
CC (CMML) characterized by abnormal clonal myeloid proliferation and
CC by progression to acute myelogenous leukemia (AML) through a
CC chromosomal translocation t(5;12)(q33;p13) that involves PDGFRB
CC and ETV6/TEL.
CC -!- DISEASE: Involved in a acute myelogenous leukemia through a
CC chromosomal translocation t(5;14)(q33;q32) that involves PDGFRB
CC and TRIP11. The fusion protein may be involved in clonal evolution
CC of leukemia and eosinophilia.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03278; AAA60049.1; -.
DR EMBL; M21616; AAA36427.1; -.
DR EMBL; U33172; AAC51675.1; -.
DR EMBL; BC032224; AAH32224.1; -.
DR PIR; A28206; PFHUGB.
DR PDB; 1GQ5; X-ray; A=1102-1106.
DR PDB; 1H90; X-ray; B=751-755.
DR PDB; 1LWP; Model; A=600-962.
DR Genew; HGNC:8804; PDGFRB.
DR H-InvDB; HIX0005310; -.
DR MIM; 173410; -.
DR GO; GO:0004992; F:platelet activating factor receptor activity; TAS.
DR GO; GO:0005017; F:platelet-derived growth factor receptor act. . .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR01824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.

